STIC-Biotech/ChemLib

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Walicka, Malgorzata

Sent:

Monday, January 14, 2002 10:53 AM

To:

STIC-Biotech/ChemLib

I would appreciate the search for:

SEQ ID NO: 1 and 2. Application No. 09/833,782, the earliest priority is 4/12/2000. Please use the pending and commercial data bases. Please RUSH!

Thank you, Malgorzata Walicka Art Unit 1652 tel.305-7270 Mali box 10C01 Room 10D06

Point of Contact: Mona Smith

that the Specialist CM1 12314 Tal: \$63-3278



STIC-Biotech/ChemLib

From: Sent:

Chan, Christina

To:

Monday, January 14, 2002 11:53 AM

Subject:

STIC-Biotech/ChemLib; Walicka, Malgorzata

FW:

Please rush. Thanks Chris

-----Original Message-----

From: Sent:

Walicka, Malgorzata

Monday, January 14, 2002 10:57 AM

To: Cc:

Chan, Christina

Subject:

STIC-Biotech/ChemLib

Christina, could you authorize this rush search?

Thank you,

Malgorzata

Searcher: M. Smith
Phone:
Location:
Date Picked Up: 1114/02
Date Completed:
Searcher Prep/Review: 10
Clerical:
Online time:

TYPE OF S	SEARCH:
NA Sequences:	
AA Sequences:_	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:_	
Othory	

VENDOR/COST(where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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Sus scrofa Adult Liver cDNA to mRNA.
VERSION
KEYWORDS
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                        Sus scrofa
REFERENCE
       JTHORS
       TTLE
                       Direct Submission
Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases.
Shigehisa Hirose, Tokyo Institute of Technology, Department of
Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama,
Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp,
Tel:045-924-5726, Fax:045-924-5824)
2 (sites)
Kato,A., Sugiura,N., Saruta,Y., Hosoiri,T., Yasue,H. and Hirose,S.
    JOURNAL
REFERENCE
    AUTHORS
                       Targeting of endopeptidase 24.16 to different subcellular compartments by alternative promoter usage J. Biol. Chem. 272 (24), 15313-15322 (1997)
    TITLE
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    MEDLINE
                        97326108
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SINE; SABP; short interspersed repeated sequence; soluble angiotesin-binding protein.
Sus scrofa (sub_apecies:domesticus) heart, liver cDNA to mRNA, clone_lib:lambdaZAP II clone:lambdaPAB[1,4,52,-L1].
Sus Scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 3819)
Sugiura, N., Hagiwara, H. and Hirose, S.
Molecular cloning of porcine soluble angiotensin-binding protein 52388174
                                                                                                                                                                                                                                                                                                                                    PIGSABP 3819 bp mRNA MAM 14-APR-2000
Sus scrofa mRNA for soluble angiotesin-binding protein, complete
                                                                                                                         2214
                                                                                                                                                          2100
                                                             2154
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Submitted (18-MAY-1992) to the DDBJ/EMBL/GenBank databases.
Shighisa Hirose, Tookyo Institute of Technology, Department of
Biological Sciences; Ookayama, Meguro-ku, Tokyo 152, Japan
(Tel:03-3726-1111(ex.2226), Fax:03-3729-0335)
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Result January 14, 2002, 18:59:51; Search time 3021.82 Seconds (without alignments) 11546.530 Million cell updates/sec US-09-833-782-1 2115 1 atgatcgcccggtgcctttt.....gaggcctgcatgctycgtga 2115 2944280 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Total number of hits satisfying chosen parameters: 1472140 segs, 8248589755 residues Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gaport 1.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 em_fun:* em_hum:* gb_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_htgo_hum:*
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	o sapiens		4000
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SUMMARIES

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                                                                                                                                                                          acctttggacatttggcagggggatacgatggccaatattatggatatctttggagtgaa 1920
 1746 TCCCTCCGAAGATTGTCAAAACATTATAAAGATGGAAGCCCTATTGCAGACGATCTGCTT 1805
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                                                                                                                                                                                                                                                                           atgctccacaatttcttgaaacgtgagccaaaccaaaaagcgttcctaatgagtagaggc
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Kapeller-Libermann, R., White, D. and Silos-Santiago, I. 22196, a novel human aminopeptidase
Patent: Wo 0123590-A 2 05-APR-2001:
Millennium Pharmaceuticals, Inc. (US)
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/db_xref="taxon:9606"
300. .2414
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Sequence 2 from Patent WO0123590.
AX106913
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                                         atgatcgcccggtgccttttggctgtgcgaagcctccgcagagttggtggttccaggatt
                                                                                            Length 2864;
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  DB
 Score 2109.4;
Pred. No. 0;
2; Mismatches
                    5
  99.78;
99.88;
                      Conservative
             Similarity
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                                                                                                     ctatattactacatgactcagacagaggaactcaagtattccatagaccaagagttcctc 1140
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aagaaaaaggaatgcaaagacaggggttttgaatatgatgggaaaatcaatgcctgggat
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/translation="MIVRCLSAARRLHRVGGSGILLRWTLGREAMSPLQAMSSYTVDG
RYNLRWDLSPPEDIKRPTELTAQTROYYDDIGALDIESTYFSKULQALADVEKYXIVE
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ELGALPDDFETDSLEKTDDLWKYKTLTKYPYFPPWKKCZIPFERRKMEMSTRTRKKEB
TILLGELPLPLRAKVRKLLGYSTHADFVLEWRYRKSTHHYTAFLDDLSGKLKPEBF
FILLNLKKKECEEKGFFYDGKINAMDLHYYMTGTEELKYSVDGEILKEYFPIEVTEG
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CFGLQPGCLLPDGSRMMSVAALVVNFSQPRAGRPSLLRHDEVRTYFHEFGHVMHQICA
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LAGGYDGQYYGYLMSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDML
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/note=-alternative product for this mRNA; oligopeptidase
:neurolysin :sBAP(soluble angiotensin-binding protein)
:MEP(microsomal metalloendopeptidase)"
                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
2340 ATGCTCCACAATTTCTTGAAACGTGAGCCAAACCAAAAGCGTTCCTAATGAGTAGAGGC 2399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases.
Shigehisa Hirose, Tokyo Institute of Technology, Department of
Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama,
Kanagawa 226-8501, Japan (B-mail:shirose@bio.titech.ac.jp,
Tel:045-924-5726, Fax:045-924-5824)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="oligopeptidase M :neurolysin :sBAP(soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kató, A., Śugiura, N., Saruta, Y., Hosoiri, T., Yasue, H. and I
Targeting of endopeptidase 24.16 to different subcellular
compartments by alternative promoter usage
J. Biol. Chem. 272 (24), 15313-15322 (1997)
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                                                                                                                                                                                                                                                                                                                                             type
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                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 2732)
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/protein_id="BAA19060.1"
/db_xref="G1:1783122"
                                                                                                                                                                                                                                   AB000170 2732 bp mRNA MAM
Porcine mRNA for endopeptidase 24.16, complete
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/db_xref="taxon:9823"
/dev_stage="Adult"
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Sus scrofa Adult Liver cDNA t
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AUTHORS
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/translation="WTLGREAMSPLQAMSSYTVDGRNVLRWDLSPEQIKRRTEELIAQ
TKQVYDDIGMLDIEEVTYENCLQALADVEVKYIVERTWLDFPQHVSSDKEVRAASTEA
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545 c 641 g 720 t ö 300 360 420 480 540 009 999 474 594 774 834 Gaps 234 294 354 414 534 654 9 gattttaacaaaaacctcaatgaggatgataccttccttgtattttccaaggctgaactt gtggaaaggaccatgctagactttccccagcatgtatcctctgacaaagaagtacgagca GACTTCAACAAAAACCTCAATGAGGACGATACCTTCCTTGTATTTTCCAAGGCTGAACTT 2732; .; 0 Length Indels 4 160; DB Score 1858.2; I Pred. No. 0; 2; Mismatches 2; 87.9%; ilarity 92.3%; Conservative 2 Similarity 826 tches 1953; Query Match Best Local S: Matches 1953; BASE COUNT ORIGIN -175 355 715 61 235 295 181 415 475 361 535 421 595 481 655 541 775 835 895 301 601 661 721 q Op QQ P Q O.Y Db oy Oy DP QY Q Óγ Ω Qy Db ò g ò g 셤 δ ò δ δ

agaaggaaggatggaaatggcttttaatacaaggtgcaaagaggaaaacaccataattttg

781

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1380 1200 1680 1560 1014 1674 960 acctttggacatttggcaggggatacgatggccaatattatggatatctttggagtgaa cagcagctactcccactgcgaaccaaggtggccaaactactcggttatagcacacatgct aagaaaaaggaatgcaaagacaggggttttgaatatgatgggaaaatcaatgcctgggat ctatattactacatgactcagacagaggaactcaagtattccatagaccaagagttcctc cctgatggaagccggatgatggcagtggctgcctcgtggtgaacttctcacagccagtg CCTGATGGGAGCCGCATGATGTCTGTGCCTGCCCTCGTGGTGAACTTCTCACAGCCACGA gaaactgactttgtagaggtgccatcgcaaatgcttgaaaattggggtgtgggacgtcgat 1375 1435 1495 1615 1741 1015 1075 1195 1255 1141 1315 1201 1261 1321 1555 1675 1735 1621 1795 1681 1855 1915 1801 1861 1135 1021 1081 1381 1441 1561 1975 955 841 961 1501 901 οχ qq QQ QQ 0y 0b g δy q ŏ Dp δy qq οy g ò g δ g οy g δy q Ωy q ŏ 合 δ

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92.3%;
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polyA_signal
repeat_unit
              variation
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Best Local 3
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TIILQELLPLRAKVAKLLGYSTHADFVLEMNTAKSTHHVTAFLDDLSQKLKPLGEAER
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 3819)
Sugiura, N., Hagiwara, H. and Hirose, S.
Molecular cloning of porcine soluble angiotensin-binding protein J. Biol. Chem. 267 (25), 18067-18072 (1992)
                                                                                                                                                                                                                                                                                                                      14-APR-2000
protein, complete
                           of
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ACTTTTGGACACTTGGCAGGGGGATATGATGGCCCAATATTATGGATATCTTTGGAGTGAA
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Substrate (sub-species:domesticus) heart, liver cDNA to rclone_lib:lambdaZAP II clone:lambdaPAB[1,4,52,-L1].
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Sus scrofa mRNA for
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VPSQMLEMWWWDTDSLRKSHYKDGSPITDDLEKLVASRLVNTGLTRQVYLSK
VDQSLHTNYSLDAASTAKTCTELLGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEV
FSMDMFYSCFKKEGIMNPEVGMKYRNLLILKPGGSLDGMDMLQNFLKREPNQKAFLMSR
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J. Biol. Chem. 272 (24), 15313-15322 (1997)
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Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases.
Shigehisa Hirose, Tokyo Institute of Technology, Department
Biological Sciences: 4259 Nagatsuta-cho, Midori-ku, Yokohama
Ranagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp,
Tel:045-924-5726, Fax:045-924-5824)
/standard_name="endopeptidase 24.16"
//note="0.1jopeptidase M :neurolysin :sBAP(soluble
angiotensin-binding protein) :MEP(microsomal
metalloendopeptidase)
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 2810)
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/db_xref="taxon:9823"
/dev_stage="Adult"

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TKQVYDDIGMLDIEEVTYENCLQALADVEVKYIVERTMLDFPOHVSSDKEVRAASTEA
DKRLSRFDIEMSMREDIFLRIVRLKETCDLGKIKPEARRYLEKSVKMGKRNGLHLPEQ
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Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases.
Shighelisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Ranagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726, Fax:045-924-5824)
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               ggacatttggcagggggatacgatggccaatattatggatatctttggagtgaagtattt
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 tactgctcagaaatattaggagttgcagctactccaggcacaaatatgccagctaccttt
                                                                           Kato, A., Sugiura, N., Saruta, Y., Hosoiri, T., Yasue, H. and F
Targeting of endopeptidase 24.16 to different subcellular
compartments by alternative promoter usage
J. Biol. Chem. 272 (24), 15313-15322 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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/protein_id="BAA19062.1"
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/db_xref="taxon:9823"
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/tissue_type="Liver"
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Sus scrofa Adult Liver cDNA
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JULS.42H - endopeptidase 24.16 type M3"

JULS.42H - BAA1905.1"

JULS.42H - BAA1905.1"

JULS.43H - BAA1905.1"

JULS.43H - BAA1906.1"

JULS.43H - BAA1906.1"

JULS.43H - BAA1906.1"

JULS.43H - BULLALADVEVKYIVERTMILDFPQHYSSDKEWRAASTEA

SREDIEMSMREDIFLARVIKETCHOLGKIRPERARYLEKSVWGKRNGILHEBQ

SREDIEMSKRANSELCIPERKNEMAFIVEKETCHOLGKIRPEDDETDELEKTDDNKYKIL

PHYFPWAKKCIPETRKMEMAFNTRCKEENTIILOEILPLRAKVAKILGYSTH

ZEMPTARTSTHHYTAFIDDISQKIKPTEGAENERETINIKKKECEEKGEPEDGKIN

ZYVKDATGELKYSVODEILKEYFPIEVTFOLLENTYGELLDISGSRAMSVAALV

ZYVKDATGEVLGOFYLDLYPREGKYNHAACFGLOFGCILPDGSRAMSVAALV

MADTSILRISKHYKDGSPITDDILEKLYASRLWTGILTLRQIVLSKVDGSLH

MADTSILRISKHYKDGSPITDDILEKLYASRLWTGILTLRQIVLSKVDGSLH

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ia; Cetartiodactyla; Suina; Suidae; Sus.
                                                      ATCCAGAGGTTGGAATGAAATACAGAAACCTAAATCCTGAAA 2164
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Tokyo Institute of Technology, Department of ces; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Japan (E-mail:shirose@bio.titech.ac.jp, Fax:045-924-5824)
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bligopeptidase M :neurolysin :sBAP(soluble nsin-binding protein) :MEP(microsomal endopeptidase)"
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3%; Pred. No. 0;
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f="taxon:9823"
aqe="Adult"
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RESULT 8
AB000174 AB000174 2604 bp mRNA MAM
DEFINITION Porcine mRNA for endopeptidase 24.16, complete cds

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TLKYPHYFPVMKKCIPETRRKMEMAFNTRCKEENTILIQELDFLRAKVAKLLGYSTH
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KSVTLYTVKRATGEVLGGFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMSVAALV
VNESQBRARRPSLLLRHDEVHTYFHEGHYMNIQICADTPREGSTWWTDVALV
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TNTSLDAASBYAKYCTEILGYAATPGTNMPAPFGHLAGGYDGQYXGYLMSBVFSNDMF
YSCFKKEGIMNDEWGMYNLIKKPGSLDGMDMLQNFLKREPNQKAFLMSRGLHAP"
478 C 594 G 712 L
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                              endopeptidase 24.16 type M3; endopeptidase 24.16 (oligopeptidase M)
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                                                                                     Euteleostomi;
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                                                                                                                                            Direct Submission Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases. Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases. Shigehisa Hirose. Tokyo Institute of Technology. Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726, Fax:045-924-5824)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 tgctgttggaatgctcggtattgaggaagtaacttacgagaactgtctgcaggcactggc
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angiotensin-binding protein) :MEP(microsomal
metalloendopeptidase)"
                                                                                                                                                                                                                                               Kato, A., Sugiura, N., Saruta, Y., Hosoiri, T., Yasue, H. and E. Targeting of endopeptidase 24.16 to different subcellular compartments by alternative promoter usage J. Biol. Chem. 272 (24), 15313-15322 (1997)
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                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 2604)

    2604
    note="corresponding to exon3,5-16 of this

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116. .2161
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                                                         to mRNA

    2604
    /organism="Sus scrofa"
    /db_xref="taxon:9823"
    /dev_stage="Adult"

                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Liver"
1. .2604
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                   Sus scrofa Adult Liver cDNA
Sus scrofa
                GI:1783131
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tes 1920; Conserv
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1345 ACAGTTCTACTTGGACCTCTATCCAAGGGAAGGAAATACAACCATGCAGCCTGCTTTGG 1404
                                                                                    1539 acgatttagcggaacaaatgtggaaactgactttgtagaggtgccatcgcaaatgcttga 1598
                                                                                                                                                                                                                                                             1599 aaattgggtgtgggacgtcgattccctccgaagattgtcaaaacattataaagatggaag 1658
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Submitted (27-DEC-1996) to the DDBJ/EMBL/GenBank databases.
Shigehisa Hirose, Tokyo Institute of Technology, Department of
Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama,
Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttatggatatcttttggagtgaagtattttccatggatatgttttacagctgttttaaaaa
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                            2019 gggatototggacggcatggacatgctccacaatttcttgaaacgtgagccaaaccaaa
                                                                                                                                               gacttactttcatgagtttggtcacgtgatgcatcagatttgtgcacagactgattttgc
                                                                                                                                                                                                                                1585 ACGATITAGTGGAACAAATGTGGAAACTGACTITGTAGAGGTGCCATCACAAATGCTTGA
                                                                                                                                                                                                                                                                                                                                   1705 CCCTATTACAGATGATCTGCTTGAAAAACTTGTTGTTGTTGTAGACTGGTCAACACAGGTCT
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Cetartiodactyla; Suina; Suidae;
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Hirose, S.
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VNFSQPRAGRPSLLRHDEVRTYFHEFCHVMHOICAOTDFARFSGTNVETDFVEVPSQM
LENWYWDTDSLRRLSKHYKDGSPITDDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLH
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BDYLEMPHYAKSTHHYTAFLDDLSOKLFVGEBREFILLIKKKREERGERGEVOKIN
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KSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMSVAALV
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                        and Hirose, S.
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/note="oligopeptidase M :neurolysin :SBAP(soluble
angiotensin-binding protein) :MEP(microsomal
2 (sites)
Kato,A., Sugiura,N., Saruta,Y., Hosoiri,T., Yasue,H. and Hargeting of endopeptidase 24.16 to different subcellular compartments by alternative promoter usage J. Biol. Chem. 272 (24), 15313-15322 (1997)
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Pred. No. 0;
                                                                                                                                                          1. 2728
/organism="Sus scrofa"
/db_xref="taxon:9823"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           metalloendopeptidase)"
                                                                                                                                                                                                                                                                                                               /note="corresponding
                                                                                                                                                                                                                                                                /tissue_type="Liver"
                                                                                                                                             Location/Qualifiers
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Matches 1921; Conservative
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Purification and characterization of a novel metalloendopeptidase
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Submitted (01-MAY-1995) F. Checler, Inst. de Pharamcologie
Noleculaire, et Cellulaire, Centre National de la Recherche
Scient., UPR 411, 660 Route des Lucioles, Sophia Antipolis, 06560
Valbonne, FRANCE
Location/Qualifiers
1. 2448
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                       gccaaatactgctcagaaatattaggagttgcagctactccaggcacaaatatgccagct 1860
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                            1834 GAÀAAACTTGTTGCTTCTAGACTGGTCAACACAGGTCTTCTGACCCTTCGCCAGATCGTT 1893
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| metalloendopeptidase; neurolysin; neurotensin-degrading neutral
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Buch, P., Vincent, J.P. and Checler, F.

Molecular cloning and expression of rat brain endopeptidase 3.4.24.1
gaaaaacttgttgcttctaggctggtcaacacaggtcttctgaccctgcgccagattgtt
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/product="neurotensin-degrading neutral
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| R.norvegicus mRNA for neurotensin endopeptidase.
| X87157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Sprague Dawley"
/db_xref="taxon:10116"
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/clone="pBluescript"
144. .258
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/note="neurolysin"
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Rattus norvegicus
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AUTHORS
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Matches 1825; Conservative
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Steven Jones, Jennifer Asano, Ian Bosdet, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Dannes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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Homo sapiens, clone MGC:3978 IMAGE:2958628, mRNA, complete cds.
BC004985
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Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Catarrhini; Hominidae;
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/tissue_type="Kidney, renal cell ad
/cione_lib="NuH_MGC_14"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
1 (bases 1 to 2637)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2646)
Strausberg,R.
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Submitted (08-JAN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                    ttgggactttcatttgaacaaatgacagatgctcatgtttggaacaagagtgttacactt 1260
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ATTACCTTAAAATATCCACACTATTTCCCTGTCATGAAGAAATGTTGTATCCCTGAAACC
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        /product-"Unknown (protein for MGC:3978)"

/brotein_id="AAH04985.1"

/db_xref="G1:13436419"

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ERRRVLEKSIKMGKRNGLHLERSPTERSKKRMSELGIDFNRNLAEDDTFLYFEXA
ELGALPHDFIDSLEKTDDDKYKITLKYPHYFPVMKKCIPFTRRMEMAFNTRCKEEN
                                                                                                         TIILQOLLPLRTKVAKILGYSTHADEVLEMNTAKSTSRVTAFLDDLSGKLKPLGEAER
BELLAUKKRECKDRGFPZOGKINAMDLYYYMGYDELKYSTDDELKEFPIEVVTEG
LLNTYOELLGLSFEGWTDAHWMKSYTLYTKDKATGEVLGOFYLDLYPREGKYNHAA
CFGLOPGCLLPDGSRWAAVALVVNFSQPVAGRPSLLHHDEVRTYFHEFGHVMHQICA
QVSFFPPPVNLPISFRKLLDCCQVSARNRFOKLNVFKNFIGLLQNQNFPYFVLFHN
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RTWLDPEQUENSENKENAASTPEADKRLSFDIEMSMRGDIEFRIVHLQETCDLGKTKTV
BARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKRRASELCIDFNKNLNEDDFFLVFSKA
ELGALLPHENDENSELEKTDDKKKITLKYPHYPPVMKKCCIPETRRRMENAFWIRCKEEN
TILLQELLPLATKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGGFAER
ELLMIYGELGLSFERCHDGSKRAMADLYYWOTGELKKYIDGFLKETPIEVYTEG
LLMIYOELLGLSFERWAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHWHQICA
QVSFFPPPNKNLLGCCQVSAANRESHLHDEVRTYFHEFGHWHQICA
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                                                                                                           Julia
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through the I.M.A.G.B. Consortium/LinL at: http://image.llnl.gov
Series: IRAL Plate: 2 Row: o Column: 6.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadann@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie For
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                      /clone="MGC:2361 IMAGE:2958628"
/tissue_1vpe="Kidney, renal cell adenocarcinoma"
/clone_lib="NIH_MGC_14"
/lab_host="DH10B-R"
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/product="Similar to thimet oligopeptidase
/protein_id="AAHO1644.1"
/db_xref="G1:12804473"
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         Project URL: http://mgc.nci.nih.gov
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Pred. No. 0;
                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                  /note="Vector: pOTB7"
126. .1949
                  Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                         Prediction of the coding sequences of unidentified human genes. XV.

The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.

NAL DNA Res. 6 (5), 337-345 (1999)

NE 20039619

C (bases I to 5343)

NES Obara, O., Nagase, T. and Kikuno, R.

Direct Submission

NDI Submitted (04-0CT-1999) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology;

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:#81-438-52-3913, Tex:#41-438-52-3914)
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                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:fh04414.
830
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Nagase,T., Ishlkawa,K., Kikuno,R., Hirosawa,M., Nomura,N.
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                                                                                                                            IAB033052 5343 bp mRNA
Homo sapiens mRNA for KIAA1226 protein,
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Conservative 2; Mismatches
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AB033052
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CATAATTTTGCAGCAGCTACTCCCACTGCGAACCAAGGTGGCCAAACTACTCGGTTATAG 120
                                                                                    121 CACACATGCTGACTTCGTCCTTGAAATGAACACTGCAAAGAGCACAAGCCGCGTAACAGC 180
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us-09-833-782-1.rge

ij

ORIGIN	Query Match Best Local Similarit Matches 1242; Conse	Qy 817 aaagaggaaac 	Oy 877 ctactcggttat	Oy 937 agccgcgtaaca	66	Db 181 GAACGAGAGTTT Qy 1057 gatgggaaatc	Db 241 GATGGGAAAATC Qy 1117 tattccatagac		361	Qy 1237 gtttggaacaag 	Oy 1297 ggacagttctat	Ay 1357 ggtctccagcct	Oy 1417 gtggtgaacttc	1477	656	Db 667 GCACGATTTAGC	Oy 1597 gaaaattgggtg 	Oy 1657 agccctattgca	Oy 1717 cttctgacctg	Qy 1777 tcgctggatgct
		oggerateggardigeredgardigerederedgardigardigeredgardiger	ydguddggccgcargcvgggga ziis 	15 AR027602 1658 bp mRNA prt		AK027602.1 GI:14042389 Oligo capping; fis (full insert sequence). Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA, clone_lib:NY2RP2_clone:NT2RP206775.	Σ					NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix	Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo. Location/Qualifiers		/clone="NT2R22005775" /cell_line="NT2" /cell_trans="nT2"	/clone_lib="WT2RP2" /clone_lib="WT2RP2" /clone_reloning vector: PuseBSFU3-mRNA from NT2 neuronal	induction." 1001245 //oct="unnamed protein product"	/coton_strt=1 /protein_id="BaB5524.1" /db_xref="GI:14042390" /translation="MNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRG	FEDOGKINANDLYYYMTQTEELKYSIDQEFIKEYFPLEVYTEGLLNYYGELLGISFEQ MTDAHVWNKSVTLYTVKOKATGEVLGGYXLDLY PREGKYNHAACFGLQPGCLLPBGSR MMAVAALVVNFSQPYAGRPSELFHDETDFARRSGTNVETDFVEVPSOMLENWWDVGS LRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASE	5 805
Db 1141 Qy 1971	Db 1201		UY 2031 Db 1321	RESULT 1 AK027602 LOCUS	DEFINITION	VERSION KEYWORDS SOURCE	ORGANISM	REFERENCE AUTHORS	9.141.19	JOURNAL REFERENCE AUTHORS	JOURNAL	COMMENT	FEATURES	source		•	CDS			BASE COUNT

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ctaccaggagttgttgggactttcatttgaacaatgacagatgctcat 1236
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                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ------AGACTGATTTT
                  54;
  Length 1658
                  Indels
Score 1178.6; DB 9;
Pred. No. 2.7e-294;
2; Mismatches 1;
 55.7%;
95.6%;
          ty 95.69
ervative
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QQ	907	TCGCTGGATGCTGCAAGTGAATATGCCAAATACTGCTCAGAAATATTAGGAGTTGCAGCT	996
ΟŊ	1837	actccaggcacaaatatgccagctacctttggacatttggcagggggatacgatggccaa	1896
QQ	196		1026
δy	1897	taltalggatalctttggagtgaagtaltttccatggatalgtttaaa	1956
οp	1027		1086
QY	1957	10 -	2016
QQ	1087	AAAGAAGGGATAATGAATCCAGAGGTTGGAATGAAATACAGAAACCTAATCCTGAAACCT	1146
Qy	2017	gggggatctctggacggcatggacatgctccacaatttcttgaaacgtgagccaaaccaa	2076
qq	1147	GGGGGATCTCTGGACGGCATGGCTCCACAATTTCTTGAAACGTGACCAAACCAA	1206
οy	2077	10 -	
Db	1207	1207 AÀAGCGTTCCTAATGAGTAGAGGCCTGCATGCTCCGTGA 1245	
Sear	ch col	Search completed: January 14, 2002, 20:25:35	
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	Run on: January 14, 2002, 18:56:01; Search (withou 955.729	Title: US-09-833-782-2 Perfect score: 3668 Sequence: 1 MIARCLLAVRSLRRVGGSRIFLKREPNQKAFLMSRGLHAP 704	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 473505 seqs, 146272329 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : SPTREMBL_17:* 1: Sp_archea:* 2: sp_bacteria:* 3: sp_fungi:*	4: sp_numan:* 5: sp_invertebrate:*	6: sp_mammal:* 7: sp_mhc:*	8: sp_organelle:* 9: sp_phage:*	12: sp_virus:*	<pre>13: sp_vertebrate:* 14: sp unclassified:*</pre>	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9byt8 homo sapien	P79433 sus scrofa	Q9bqd0 homo sapien	Q9ul14 homo sapien	Q9epx1 mus musculu	Q9ptv2 xenopus lae	Q9bw75 homo sapien	P97996 asperdillus	Q9fxd5 arabidopsis	Q9kvf8 vibrio chol	Q9la87 aeromonas h	Q9i765 pseudomonas	Q9cmx1 pasteurella	Q9kle2 neisseria m	Q91x57 neisseria m	P74571 synechocyst	091s13 arabidopsis	Q9rtu7 deinococcus	091xa6 arabidopsis
SUMMARIES	ID	Q9BYT8	P79433	09BQD0	Q9ULJ4	Q9EPX1	Q9PTV2	Q9BW75	P97996	Q9FXD5	Q9KVF8	Q9LA87	091765	Q9CMX1	Q9K1E2	Q9JX57	P74571	09LSL3	Q9RTU7	09LXA6
	DB	4	9	4	4	11	13	4	m	10	7	7	7	7	7	7	7	10	7	10
	% Query Match Length DB	704	745	607	447	687	685	480	716	866	089	680	681	.649	678	678	713	714	685	723
	& Query Match	100.0	93.8	72.0	64.2	62.7	62.5	46.4	32.1	27.7	23.1	21.9	21.7	21.3	19.1	18.9	18.8	18.6	18.3	17.3
	Score	3668	3441	2640	2355	2299	2291.5	1703	1177	1017.5	848	804	794.5	781.5	702	694	690.5	681.5	671.5	635.5
	Result No.		7	m	4	5	9	7	œ	6	10	11	12	13	14	15	16	17	18	19

Q9ph19 xylella fas	Q9pc41 xylella fas	Q9v9h7 drosophila	Q9a264 caulobacter	Q9cyn6 mus musculu	O60982 leishmania	Q9cul3 mus musculu	Q9vc06 drosophila	Q9p450 schizophyll	Q9nlt5 leishmania	062512 caenorhabdi	Q9kq15 vibrio chol	Q991k5 mus musculu	Q9kfv0 bacillus ha	_	051465 borrelia bu	Q9x1x1 thermotoga	Q26223 plasmodium	O83423 treponema p	Q9uzc8 pyrococcus	Q9zm03 helicobacte	O61566 ascaris suu		Q9c1q0 kallichroma	Q9x058 thermotoga	
2 Q9PH19	2 Q9PC41	5 Q9V9H7	2 Q9A264	11 Q9CYN6	5 060982	11 Q9CUL3	5 Q9VC06	3 Q9P450	5 Q9NLT5	5 062512	2 Q9KQL5	11 Q99LK5	2 Q9KFV0	5 Q9BJX9	2 051465	2 Q9X1X1	5 026223	2 083423	1 Q9U2C8	2 Q92M03	5 061566	5 Q9V4F2	3 Q9C1G0	2 Q9x058	
674	716	669	677	711	678	93	730	265	127	820	615	81	532	2747	2166	852	2269	1084	880	578	1095	167	3734	547	
17.1	15.8	15.2	15.1	13.8	13.5	13.0	12.3	7.3	5.2	5.2	4.8	4.5	3.9	3.9	3.8	3.8	3.8	3.8	3.7	3.7	3.7	3.7	3.7	3.6	
627.5	578.5	556	553	507.5	495.5	478	452.5	268.5	191.5	189	175.5	166	143	141.5	140	139.5	139.5	139	137.5	135	135	134	134	133	
20	22	23	24	25	36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

	· 0		
SUL	EMBL; AJ300837; CAC27329.1; Hydrolase. Hydrolase. SEQUENCE 704 AA; 80651 MW; 80136688D79BBEDF CRC64; Subject Match 100.0%; Score 3668; DB 4; Length 704; Best Local Similarity 100.0%; Pred. No. 2.4e-229; Matches 704; Conservative 0; Mismatches 0; Indels 0; Gaps	QY 1 MIARCLLAVRSLRRVGGSRILLRWILGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR 60 1	OY 121 ASTEADKRLSRFDIEMSWRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKWGKRNGLHL 180 121 ASTEADKRLSRFDIEMSWRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKWGKRNGLHL 180 OY 181 PEQVQNEIKSWKRRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK 240 181 PEQVQNEIKSWKRRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK 240 181 PEQVQNEIKSWKRRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK 240 181 PEQVQNEIKSWKRRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK 240

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RX MEDLINE-97326108; PubMed-9182559;

RA FASTO A., Sugiura N., Sautta Y., Hosoiri T., Yasue H., Hirose S.;

RA Fatto A., Sugiura N., Sautta Y., Hosoiri T., Yasue H., Hirose S.;

RT Gompartments by alternative promoter usage.";

J. Bid. Chem. 272:15313-1532(1997).

RL J. Bid. Chem. 272:15313-1532(1997).

RL J. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);

CC ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.

DR EMBL; AB000172; BAA19066.1; -

DR EMBL; AB000173; BAA1906.1; -

DR EMBL; AB000175; BAA1905.1; -

DR EMBL; AB000415; BAA19105.1; JOINED.

DR EMBL; AB000414; BAA19105.1; JOINED.

DR EMBL; AB000415; BAA19105.1; JOINED.

DR EMBL; AB000417; BAA19105.1; JOINED.
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                                                                         LYYNMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL 420
                                                                                                                         601 AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
                        DEVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
                                                                                                                                                                                                               AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
                                                                                                                                                                                                                                                               SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
                                                                                                                                                                                                                                                                             241 ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                          661 VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             661 VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
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JOINED.
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BAA19105.1;
BAA19105.1;
BAA19105.1;
BAA19105.1;
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AB000424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 VTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 FYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 IADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEILGVAATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 GTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSELCIDENKNINEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYKITLKYPHYFPVMKK
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                                                                                                                                                                                                                                                                                                                            Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Metalloprotease; Hydrolase; Zinc.
SEQUENCE 745 AA; 85109 MW; EC451B8EAD4AC28F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                         93.8%; Score 3441; DB 6; 95.1%; Pred. No. 1.3e-214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
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EMBL; AB000170; BAA19061.1; --
EMBL; AB000171; BAA19062.1; --
EMBL; AB000172; BAA19062.1; --
EMBL; AB000425; BAA19106.1; --
EMBL; AB000414; BAA19106.1; --
EMBL; AB000414; BAA19106.1; JOINED.
EMBL; AB000416; BAA19106.1; JOINED.
EMBL; AB000416; BAA19106.1; JOINED.
EMBL; AB000419; BAA19106.1; JOINED.
EMBL; AB000419; BAA19106.1; JOINED.
EMBL; AB000420; BAA19106.1; JOINED.
EMBL; AB000421; BAA19106.1; JOINED.
EMBL; AB000422; BAA19106.1; JOINED.
EMBL; AB000424; BAA19106.1; JOINED.
EMBL; AB000424; BAA19106.1; JOINED.
EMBL; AB000424; BAA19106.1; JOINED.
EMBL; AB000424; BAA19106.1; JOINED.
INTERPO; IPR00130; ZO, MTPEPTOS.
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Best Local Similarity
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SLDGMDMLQNFLKREPNQKAFLMSRGLHAP 745

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241 EFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIAD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 FLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFH 497
                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIAD
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                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.2%; Score 2355; DB 4; Length 447; 100.0%; Pred. No. 1.3e-144; ive 0; Mismatches 0; Indels
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                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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                                                                    Created)
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InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPR001567; Peptidase_M3.
                                                                                                                                                                                                                                                                             MEDLINE=20039619; PubMed=10574462;
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                            Q9ULJ4;
Q9ULJ4;
01-MAY-2000 (TEMBLFel. 13,
01-MAY-2000 (TEMBLFel. 13,
01-JUN-2001 (TEMBLFel. 17,
                                                                                                                   KIAA1226 PROTEIN (FRAGMENT)
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                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                               TISSUE=BRAIN;
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SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:3978) (SIMILAR TO THIMET OLIGOPEPTIDASE 1).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIARCLLAVRSLRRVGGSRILLLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.0%; Score 2640; DB 4; Length 607; 94.8%; Pred. No. 7.1e-163; tive 4; Mismatches 14; Indels 10
                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004985.1; -.
EMBL; BC001644; AAH01644.1; -.
SEQUENCE 607 AA; 70304 MW; 1CB7DEAF29A6B2C3 CRC64;
                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                  607 AA
                                                  PRT;
                                                                                                                                                                                                                                                           IISSUE=KIDNEY ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-KIDNEY ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.0
Best Local Similarity 94.8
Matches 514; Conservative
                                                PRELIMINARY;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                         NCBI_TaxID=9606;
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|DFLISLEKAEDGKLKVTLKYPHYFPLLKKCHVPETRRLLEEAFNCRCKEENCAILKELVS 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKEC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 KDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSF 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQMIDAHVWNKSVILYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSR 465
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                                                                                                                                                                                                                                                                                                                                                                                                                           22 NHLRWDLSAQQIRALTTQLIEQTKCVYDRVGAQNFEDVSYESTLKALADVEVTYTVQRNI 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEKSIKMGKRNGLHLPEQVQNEIKSMKRRMSELCIDFNKNLNEDDTFLVFSKAELGALPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                     Glucksman M.J.; "The Neuropeptide Processing Enzyme EC 3.4.24.15 Is Modulated
                                                                                                                                                                                                                                                                                                                                                              Length 687;
                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-20538378; PubMed=10969067; Tullai J.W., Cummins P.M., Pabon A., Roberts J.L., Lopingco Shrimpton C.N., Smith A.I., Martignetti J.A., Ferro E.S.,
                                                                                                                                                                                                                                                                                                                        687 AA; 77994 MW; F34A63D7C2A6D018 CRC64;
         01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01.5UN-2001 (TrEMBLrel. 17, Last annotation update)
THIMET OLIGOPEPTIDASE (EC 3.4.24.15).
                                                                                                                                                                                                                                                                                                                                                           62.7%; Score 2299; DB 11;
64.8%; Pred. No. 1e-140;
Live 92; Mismatches 139;
                                                                                                                                                                                                                                                           InterPr'o: IPR001567; Peptidase_M3.
InterPr'o: IPR000130; zn_Myrpeptdse.
Pfam: PF0143; Peptidase_M3; I.
PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_I
                                                                                                                                                                                                           Protein Kinase A Phosphorylation.";
J. Biol. Chem. 275:36514-36522(2000)
EMBL; AF314187; AAG35061.1; -:
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 64.8%
nes 425; Conservative
                                                                                                                                                                                                                                                MGD; MGI:1354165; Thop1.
                                                                        musculus (Mouse)
                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                             Hydrolase.
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 LRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKEC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 LDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 EOMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 LEKSIKMGKRNGLHLPEQVQNEIKSMKRMSELCIDFNKNLNEDDTFLVFSKAELGALPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466 MMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFV
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                          646 MFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okida N., Ishikawa K., Tokumoto M., Tokumoto T.;
"Xenopus thimet oligopeptidase.";
"Xenopus thimet oligopeptidase.";
submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB0309041; BA989309.1;
InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPR001567; Peptidase_M3.
Pfam; PF01432; Peptidase_M3. I.
PROSITE; PS00142; ZINC_PROPEASE; UNKNOWN_1.
SEQUENCE 685 AA; 78137 MW; F41C5EE45BBB78ED CRC64;
                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 13, Last sequence update)
THIMET OLIGOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     le-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.5%; Score 2291.5;
64.4%; Pred. No. 3.1e
iive 98; Mismatches
                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity 64.4%; 426; Conservative
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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LADVEVKYIVERTMLDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIF---ERIVH 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQ 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 PIEVVTEGLLNTYQELLGLSFEQMTDAH------VWNKSVTLYTV-KDKATGE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:: ||:| ::| || || ::| | PLQTTIEGMLKIFEELFGLVFVEITGEDREKVAPTGKGSDIVWHEDVQVFSVWNDEGEGS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 -VLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRH 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHT 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 NTS-----LDAASEYAKYCS-----EILGVAATPGTNMPATFGHLAGGYDGQYYGY 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 PLQAMSSYTVAGRNVLRWDLSPEQIKTRTEELIVQTKQVYD-AVGMLGIEEVTYENCLQA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PPQAPPLFTATAQSIV------DDAKRLIETSRKVRDNIVANVKPESATFDSVLKP 58
                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 LQETCDLGKIKPEARRYLEKSIKMGKRNGLHLPE-QVQNEIKSMKKRMSELCIDFNKNLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 KLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.1%; Score 1177; DB 3; Length 716; Best Local Similarity 37.7%; Pred. No. 4.9e-68; Matches 273; Conservative 125; Mismatches 253; Indels 7
                                                                                                                                                                                                                         Ibrahim-Granet O., d'Enfert C.; The Appergillus fumigatus mepB gene encodes an 82 kba intimetaloproteinases tructurally related to mammalian thimet oligopeptidases."; Microbiology 143:0-0(0).

EMBL; U85769; AAB6656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              00142; ZINC_PROTEASE; UNKNOWN_1.
716 AA; 81923 MW; 6480A86C90185322 CRC64;
                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTRACELLULAR METALLOPROTEINASE MEPB.
                                                                                                     Aspergillus fumigatus (Sartorya fumigata).
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; U
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001567; Peptidase_M3.
                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97388579; Pubmed-9245813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVV 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSL 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKE 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-NEUROBLASTOMA;
Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: BC000583; AAH00583.1; -.
SEQUENCE 480 AA; 54735 MW; 96250597AC877913 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL 701
                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.4%; Score 1703; DB 4;
65.5%; Pred. No. 2.4e-102;
tive 68; Mismatches 93;
                                                                                                                                                                                                                                          480 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 716
                                                                                                                                                                                                                                                                          Created)
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Best Local Similarity 65.55
Matches 306; Conservative
                                                                                                                                                                                                                                       PRELIMINARY;
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RESULT P97996 ID P9

112949 MW; 49CBE1C8225955E8 CRC64;

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998 AA;
SEQUENCE
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                                              SEQUENCE FROM N.A.
Cheuk'R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
                              637 LWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFL 696
                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Arabidopsis thaliana BAC F12A21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                  Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C!, Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 593 AESHEQIQKLPISTTYNQLRKQIALQDGPEVLGMGDEWG-HGEATFGHLIGGYDAGYYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theologis A., Ecker J.;
Theologis A., Ecker J.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC008113; AAG28905.1;
Intenpro; IPR001567; Peptidase_M3.
Interpro; IPR00130; Zn_MTpeptdse.
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
F12A21.16.
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                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                         711 KELGL 715
                                                                                          697 MSRGL 701
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SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449
                                                                                                                 51 DLSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQ 110
                                                                                                                                                                                                                             111 HVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSI 170
                                                                                                                                                                                                                                                                331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 EYDGKI--NAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQM 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 TDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMA 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 SQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSL 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 SQLLENW------QDITK-----PLVDEVCKTLKRWRYSFSALKSLQEILYCLFDQII 556
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                           171 KMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 ACVCGYAHFADYALDRRMSKTSMRVIRFLEDISSSLTDLAIREFSILEDLKRKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 VALLIAQFAKDGSGEAVPLGFSDVVNLFHEFGHVVQHICNRASFARFSGLRVDPDFREIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557 YSDDDADLLQLIRSLHPKV---MIGLPVVEGTNPASCFPRAVIGSEATCYSRLWSEVYAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 AKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 HINTSLD----AASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
  Length 998;
                                                             Matches 221; Conservative 157; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
Score 1017.5; DB 10;
Pred. No. 1.7e-57;
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     27.78;
33.78;
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        Query Match
Best Local Similarity
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01-OCT-2000 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                    Aeromonas.
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Best Local S
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                                                                                                                                                                                                                                                       VVNSDELREAYESCLPLLSEYSTWVGQHKGLFEAYKTIKESAEFAKLDRAQQKNISDSLR 135
                                                                                                                                                                                                                                                                                 MGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKA-----ELGALPDD 226
                                                                                                                                                                                                                                                                                                  DFELSGIGLPLOEOKRYGEISKRMSELGSKFSNNVL--DATMGWTKQITDVNLLAGMPES 193
                                                                                                                                                                                                                                                                                                                                                                             FSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGL 573
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                                                                                                                                                                                                                                                                                                                                                                                                            EFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLL 394
                                                                                                                                                                                                                                                                                                                                                                                                                         VSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIK 171
                                                                                                                                                                                                                                                                                                                                             194 ALAAAQAAAEAKGLEGYLLTLDIPSYLPVMTYCDNQALRKEVYEAYVTRASDRGPNAGKW 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGL 454
                                                                                                                                                                                                LSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQH 111
                                                                                                                                                                                                             Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.
                                                                                                                                                                                                                                                                                                                         FIDSLEKTDDDK----YKITLKYPHYFPVMKKCIPETRRMEMAFNTRC-----KE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574 LTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI-LGVAATPG---TNMPATFGHL-AGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                         Length 680
                                                                                                                                                     'Match 23.1%; Score 848; DB 2; Length 66 Local Similarity 31.0%; Pred. No. 9.1e-47; les 209; Conservative 128; Mismatches 304; Indels
                                                                                                             Complete proteome. sequence 680 AA; 77034 MW; EFC0BE85B6D12C9E CRC64;
                                                                                         Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1
                                                                   InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; In_MTpeptdse.
                                    Nature 406:477-483(2000).
EMBL; AE004109; AAF93364.1;
TIGR; VC0188;
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                               cholerae.
                                                                                                                                                       Query Match
                                                                                                                                                                          Matches
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116 SDDFPLLSAAQRKEIQNTLRDFRLSGIGLPAEAQQRYGEIQARLSELASRFSNNVLDATQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEEVNDRLSRIWSPVSHLNSVLNSEALREAHDACLPLLSEFQTYVGQHEGLYQAYLALSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 EMAFNTRC-----KEENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYD----GKINAWDLYYYMTQTEELK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 YSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVL 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 GWSKLVTDEAELAGLPASAQAAARQLAELKGKEGWLFTLDIPSYLPVMMYADNRALRAEL 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NPLLTMDSLPPFSQ-----IQPDQVQPAVTQAIADCKQKISDV-LAQREPHTWDSLIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LADVEVKYIVERTMLDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQE
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                                                                                                                                                                                                                                                            STRAIN-PPD134/91;
MEDLINE-20244644: PubMed-10784058;
Zhang Y.L., Ong C.T., Leung K.Y.;
"Molecular analysis of genetic differences between virulent and avirulent strains of Aeromonas hydrophila isolated from diseased fish.";
                                                                                     Aeromonas hydrophila.
Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.9%; Score 804; DB 2; Length 68 ilarity 30.7%; Pred. No. 6.5e-44; Conservative 119; Mismatches 316; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF146608; AAF45039_1, -
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01432; Peptidase_M3, 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SEQUENCE 680 AA; 76602 MW; D8E498F7D93D9A2B CRC64;
Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, PUTATIVE OLIGOPEPTIDASE A.
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215; Conserv
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=644;
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KYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHA 703

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09LA87; 01-OCT-2000 (TrEMBLrel. 15, Created)

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429 RRRDAQGRLIDPVAYLVCNFTPAVNGKPALLTHDEVTTLFHEFGHGLHHLLTRVEHAAAS 488
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EMBL; AR005104; ARA02764.1; -.
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                          517 GTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLT
                                                                                                                                                                      576 LRQIVLSKVDQSLHTNTSLDAAS--EYAKYCSEILGVAATPGTNMPA-TFGHL-AGGYDG
                                                                                                                                                                                                                                                                                   632 QYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPN
                                                                                       172 MGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTF----LVFSKAELGALPDDF
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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Last annotation update)
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Complete proteome.
SEQUENCE 679 AA: 77545 MW; 324654130205
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MEDLINE=21145866; PubMed=11248100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PAO1:
MEDLINE=20437337; PubMed=10984043;
StOVET C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
StOVET C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 IRPEHVKPAIERILADNRAAIARLLETQREQPTWKGLVLAMDELNDRLGAAWSPVSHLNA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 GPVWEEILDLRQELAGLLGFANYAELSLATKWAESSDQVLSFLRDLAVRSKPFAARDLEQ
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                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
  Query Match 21.7%; Score 794.5; DB 2; Best Local Similarity 30.1%; Pred. No. 2.7e-43; Matches 202; Conservative 132; Mismatches 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL, AE004446; AAG03457.1;
InterPro; IPR0011567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, OLIGOPEPTIDASE A.
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
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SEQUENCE 681 AA
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091765;
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A Parkhill J. Achtman M., James K.D., Bentley S.D., Churcher C.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
A pagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
menigitidis 22491.";
"Mature 404:502-506(2000).
R BMBL; AL162752; CAB83371.1; -.
R InterPro; IPRO01567; Peptidase_M3.
R InterPro; Peptidase_M3: 1.
R Pfam. PF01422; Peptidase_M3: 1.
R Hydrolase; Complete proteome.
SEQUENCE 678 AA; 76013 MM; 6217B1E603D3C51 CRC64;
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                                                                    EKSIKMGKRNGLHLPEQVQNEIKSMKRRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505 QICAQTDFARFSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSP1ADDLLEKL 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 VASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TFGHL-AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                      251 KFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDLARRAKPYAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 KYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMH
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
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STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
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STRAIN=MC58 / SEROGROUP B;

STRAIN=2017575; PubMcd=10710307;

Tettelln H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Heod D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., Deaboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksy D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Glil J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                      ELIQRIFNIRTVERFGIDTWHNDVRFFDLIDE-NDNLRGSFYLDLYARENKRGGAWMDDC 425
                                                                                                                                                                                                                                                                                                                                                                                                                     571 TGLLTLRQIVLSKVDQSLH-----TNTSLDAASEYAKYCSEILGVAATPGTNMPATFG 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 EQIKTRTEELIVQT -- KQVYDAVGMLGIEEVT -YENCLQALADVEVKYIVERT -- -- ML 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=491;
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                                                                                                 NTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHA---AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 AAMFVLROLEFGLFDFRLHHFDPTKANOILDTLKAVKEEVAVIKGV---EWARAPHSFS
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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EMBL; AE002379; AAF40670.1;
TIGR; NMB0214:
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                                                                                                                                                                                                                                                   224 PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKE---- 274
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                                                                                                                                                                                       167 EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
                                   Gaps
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Length 678;
 , Match 18.9%; Score 694; DB 2; Length 67 Local Similarity 28.2%; Pred. No. 8.5e-37; les 190; Conservative 131; Mismatches 309; Indels
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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	75				AAA81287	N. meningitidis
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660 gcaagtacagaagcagacaaaagactttctcgttttgatattgagatgagcatgagagga

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cancer, and

and lung

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This sequence represents cDNA encoding a novel human aminopeptidase, designated 22196. cDNA clones encoding human aminopeptidase 22196 were identified in a bone marrow cDNA library using an EST (expressed sequence tag) selected on the basis of homology to aminopeptidase 22196 is thought to be a metalloenzyme, as it contains a zinc-binding region signature found in neutral zinc metallopeptidases. Expression analysis indicated that the aminopeptidase is highly expressed in normal osteoblasts, testis, skeletal muscle, foetal kidney and foetal liver. It is also expressed in normal brases, lung, and colon tissue, and is overexpressed in lung and colon cancer. Expression was found to be downregulated during stromal cell osteoblast lineage naturation. Aminopeptidase 22196 may be used to treat pain, and cancers of the lung and colon. It can also be used in drug screening to identify compounds which bind to it and modulate its activity. Such compounds may be used in the treatment of a wide variety of conditions, including and colon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      consequence of a variety of controlled in the control of seases (e.g., splenomegaly); infectious diseases (e.g., malaria, tuberculosis); immune disorders (e.g., rheumatoid arthritis, systemic lupus erythematosus, acquired immunodeficiency syndrome (AIDS)); lung disorders (e.g., pulmonary embolism, emphysema, bronchial asthma; colon disorders (e.g., diarrhosa, Crohn's disease, ulcerative colitis); liver disorders (e.g., hepatic cirrhosis, hepatitis); uterine disorders (e.g., diarrhosa, crohn's disease, meningitis, Alzheimer's disease, Parkinson's disease, Huntington's disease); skin disorders (e.g., wholligo urticaria, skin tumours, psoriasis); cardiac and sacchat disorders (e.g., myocardial infarction, chronic ischaemic heart disease, hypertension, atherosclerosis); and one disorders (e.g., osteoporosis, Paget's disease). Nucleotides encoding aminopeptidase 22196
                                                                                                                          used to treat colou a
treat e.g. cirrhosis
Silos-Santiago
                                                                                                                                                                                                            Claim 3; Fig 1A-C; 109pp; English
White D,
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                                                                                                                             Novel human aminopeptidose,
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Kapeller-Libermann R,
                                                 2001-300101/31
)B; AAB73485.
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Sequence 2864 BP; 854 A; 556 C; 693 G; 761 T; 0 other;

ö accgtggctggcagaaatgttttaagatgggatctttcgccagagcaaattaaaaacaaga 479 240 gigaaaaggaccatgctagactttccccagcatgtatcctctgacaaagaagtacgagca 360 629 gcaagtacagaagcagacaaaagactttctcgttttgatattgagatgagcatgagagga 420 ttactcagaatgacgttaggaagagaagtgatgtctcctcttcaggcaatgtcttcctat 120 ttactcagaatgacgttaggaagaagtgatgtctcctcttcaggcaatgtcttcctat 419 gaggaagtaacttacgagaactgtctgcaggcactggcagatgtagaagtaaagtatata 300 actgtggctggcagaaatgttttaagatgggatctttcaccagagcaaattaaaacaaga actgaggageteattgtgcagaccaaacaggtgtacgatgctgttggaatgctcggtatt 22; Length 2864; ö Indels BB 99.7%; Score 2109.4; 99.8%; Pred. No. 0; iive 2; Mismatches Best Local Similarity 99.8 Matches 2110; Conservative Query Match 61 360 420 180 540 301 121 181 361 g g ò g g ద ò ò g ò ç οy

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/note= "the identity of many
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                                                                                                                                                                                                                                                                                The rabbit endopeptidase was purified from rabbit liver and digested with CNBr. Families of degenerate primers were designed based on the amino acid sequences of the CNBr fragments. The primers were used to amplify sequences from a rabbit cDNA library. An amplified fragment was isolated and used to probe the same library. Two overlapping clones produced a 2148bp sequence. A preliminary sequence are unassigned; the actual amino and 5' and 3'-most sequences are unassigned; the actual amino and carboxil terminals of the protein have not yet been determined. The short untranslated 5' and 3' sequences are primer sequences see AAR26107-R26113 and AAQ27305-Q27307.
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID 11796; 2537pp + CD ROM; English.
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                 cttcttgaaaancttgttgcttctagactggtcaacacaggtcttctgacccttcgccag 1906
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                                                             attgttttgagcaaagttgatcagtctttcataccaacacatcgctggatgctgcaagt
Yamamoto
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, Otsuki
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A, Nagai
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T, Wakamatsu
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0241899.
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CC polynucleotide which comprises a 3'-end sequence, where the cligonucleotide comprises at least 15 nucleotides and the combination of the sequence's'-end sequence! is selected from those defined in the sequence's'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC chefull-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13639 represent human cDNA sequences; AAH36246 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 corpresent oligonucleotides, all of which are used in the exemplification XX Sequence 1658 BP; 508 A; 308 C; 374 G; 468 T; 0 other;

ï ggtctccagcctggctgccttctgcctgatggaagccggatgatggcagtggctgcctc 1416 ggacagttctatttggacctctatccaagggaaggaaaatacaatcatgcggcctgcttc 1356 gaacgagagtttattttgaatttgaagaaaaaggaatgcaaagacaggggttttgaatat 1056 tattccatagaccaagagttcctcaaggaatacttcccaattgaggtggtcactgaaggc 1176 gtttggaacaagagtgttacactttatactgtgaaggataaagctacaggagaagtattg 1296 aggacttactttcatgagtttggtcacgtgatgcatcagatttgtgcacagactgatttt 1536 gaacgagagtttattttgaatttgaagaaaaaggaatgcaaagacaggggttttgaatat 240 aaagaggaaaacccataattttgcagcagctactcccactgcgaaccaaggtggccaaa 876 ctactcggttatagcacacatgctgacttcgtccttgaaatgaacactgcaaagagcaca 936 ctactcggttatagcacacatgctgacttcgtccttgaaatgaacactgcaaagagcaca 120 agccgcgtaacagcytttctagatgatttaagccagaagttaaaacccttqqqtqaaqca 996 Gaps ggacagttctatttggacctctatccaagggaaggaaaatacaatcatgcggcctgcttc gtggtgaacttctcacagccagtggcaggtcgtccttctctctgagacacgacg----.----gactgatttt 54; Length 1658 Indels Sequence 1658 BP; 508 A; 308 C; 374 G; 468 T; 0 other; 22; 1; DB Score 1178.6; Pred. No. 0; 2; Mismatches 2; 55.7%; Matches 1242; Conservative Similarity Query Match Local 817 1057 1117 1177 541 601 1477 1537 877 937 121 166 241 301 361 1237 421 1297 481 1357 1417 299 61 181 d οq pp δý g οy Ор ò q οy g Ω qq g δ g οχ ò a δÿ ò ŏ q ŏ

1776 1147 gggggatctctggacggcatggacatgctccacaatttcttgaaacgtgagccaaaccaa 1206 gaaaattgggtgtgggacgtcgattccctccgaagattgtcaaaacattataaagatgga gaaaattgggtgtgggacgtcggttccctccgaagattgtcaaaaacattataaagatgga cttctgaccctgcgccagattgttttgagcaaagttgatcagtctttcataccaacaca tcgctggatgctgcaagtgaatatgccaaatactgctcagaaatattaggagttgcagct actccaggcacaaatatgccagctacctttggacatttggcagggggatacgatggccaa aaagaagggataatgaatccagaggttggaatgaaatacagaaacctaatcctgaaacct 99999atctctggacggcatggacatgctccacaatttcttgaaacgtgagccaaaccaa PA; zinc; Seubert protein; APP; 'n aaagcgttcctaatgagtagaggcctgcatgctccgtga 1245 McConlogue aaagcgttcctaatgagtagaggcctgcatgctycgtga 1..2070 /*tag= a /product= amyloidin_protease Alzheimer's disease; beta amyloid precursor metalloprotease; hAP; protease inhibitor; ss Human amyloidin protease coding sequence. SP, Location/Qualifiers BP. Little (ATHE-) ATHENA NEUROSCIENCES INC (ELIL) LILLY & CO ELI. 900S-0594122. 91WO-US07290 (first entry) standard; cDNA; EM, Johnstone WPI; 1992-167148/20 Homo sapiens 04-OCT-1991; 30-SEP-1991; 09-NOV-1992 05-OCT-1990; WO9207068-A 30-APR-1992 HE, AAQ24875 AAQ24875; ŝ Dovey Sinha 4 1087 1657 1717 1777 1837 1897 1027 1207 1597 727 787 847 907 196 AAQ24875 Key RESULT Dρ СP qq qq Ωÿ g δ g δ qq δŽ Q ŏ a δ δ Óγ

P-PSDB;, AAR24259

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The complete sequence of the human amyloidin gene was obtained by sequencing two clones: clone cHL57 (codons 1-480) and clone cHL53 (codons 1-480) and clone cHL53 (codons 1-480) and clone cHL53 long two clones: clone cHL65 (codons 1-480) and clone cHL63 (codons 1-480) and clone cHL63 superior cannot be colored to the following sources: normal human brain, superior temporal gyrus and human embryonic kidney cell line 293. Examination of the nucleotide sequence reveals that there is no clear hydrophobic leader sequence. The deduced amino acid sequence of the amyloidin protease contains the motif X-H-E-F-G-H-X at the active site typical of zinc-dependent metallopeptidases; the two histidine residues coordinate the Zn (2+) in the active centre and the glutamate is involved in bond-breaking.
                                                Human amyloidin protease – used for cleaving Met-Asp bond :
amyloid-like substrate for identifying protease inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the glutamate is involved in bond-breaking.
See also AAR24260-3, AAR24266-7 and AAQ24876-Q24887
                                                                                                                                English.
                                                                                                                                Claim 37; Page 53-54; 62pp;
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CDNA

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Sequence 2070 BP; 434 A; 626 C; 678 G; 332 T; 0 other;

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716 aagtggaggaggcettcaactgccggtgcaaggaggagaactgcgctatcctcaaggagc 775
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The present invention describes primer sets for synthesising 5602
[ull-length cDNAs defined in the specification. Where a primer set
comptriess: (a) an oilgo-dr primer and an oilgouncleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide which comprises as 1'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length without any specialised methods. AAH1318 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                      1916 tggattacagaagctgcatcctgagacccggcggttccgaggatgccagcgccatgctga 1975
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  ccatggatatgtittacagctgttttaaaaaaagaagggataatgaatccagaggttggaa 1987
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Otsuki
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A, Nagai K,
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Wakamatsu
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Ishii S, Sugiyama T, Wakama
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                                                          29.2%; Score 618.4; DB 22 98.4%; Pred. No. 2.5e-169;
                                           Sequence 776 BP; 227 A; 172 C; 174 G; 190 T; 13
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                      of the present invention.
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Human colon cancer cell line Km12L4-A cDNA library derived sequence #982.

(first entry)

27-JUL-2001

Human; diagnosis; colon cancer; cancer; malignant; chromosome mapping; detection; colon cancer cell line ${\tt Km12L4-A}$; ss.

WO200018916-A2 Homo sapiens.

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The present invention describes a library of polynucleotides comprising not by a pulled sequences (given in AAH30067 to AAH3145). Also described are: (1) an isolated polynucleotide (1) having at least 90% identity to one of the 1079 sequences; (2) a recombinant host cell containing (1); (3) an isolated polypeptide (11) encoded by (1); (4) an antibody that specifically binds to (11); (5) a vector comprising (1); and (6) a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell comprising detecting a gene product encoded by 65 fthe 1079 sequences given in the specification. The polynucleotides are used to monitor patients having (or susceptible) to cancer to detect potentially malignant events at a molecular level before they are contextable at a gross morphological level. The polynucleotides are also useful for monitoring the efficacy of various therapies and preventive interventions. Polynucleotide probes based on the disclosed sequences are used to useful for chromosome mapping and detection of transcription levels. The 1079 polynucleotide sequences were derived from a human colon cancer colon line Km12L4-A cDNA library.
                                                                                                                                                                                                                                               C, Pot D, Kassam A;
n M, Drmanac S, Labat I;
Stache-Crain B;
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Randazzo F, Kennedy GC, Fv
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Stach
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                                                                                  98US-0102180.
98US-0102380.
98US-0103815.
                                   99WO-US22226
                                                                      98US-0102161
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Reinhard C, Giese K, Rand
Lamson G, Drmanac R, Crk
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Best Local Similarity
Matches '339; Conserv
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                                 23-SEP-1999;
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                                                                      28-SEP-1998
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06-APR-2000
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proteins, called pancreatic cancer antigens, given in AAB54008 to
AAB54466. The human pancreatic cancer antigens have cytostatic,
concurportective, nootropic, immunomodulatory, relaxant, contraceptive,
concurportective, nootropic, immunomodulatory, activities, and can be used
concurportective, nootropic, immunomodulatory, activities, and can be used
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concurportective and antigens to the proteins and the activity of the
concurportective and antigens to the antigens can be used to design nucleic
concurportective antigen polynucleotides can be used to design nucleic
acid hybridisation probes that can be used in chromosome mapping, linkage
and liagnostic methods. The proteins can be used to generate antibodies
which are used to purify, detect and target the polypeptides, including
contrains can be used to purify the proteins can detect and therapeutic methods. The
contrains can be used to purify the proteins can detect and therapeutic methods. The
contrains can be used to purify the protein contrains to the proteins can detect and therapeutic methods. The
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                                                                                                                                                                                                                                 Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                     Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:25.
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                                               BP,
                                               AAC98797 standard; cDNA; 900
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P-PSDB; AAB54032.
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Length 900;

DB 21;

14.6%; Score 308.8; DB 21; Length 64.1%; Pred. No. 2.3e-79; Live 0; Mismatches 268; Indels

480; Conservative

Similarity

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                 ctgcagaconcaggtctgcggcaggatgggagccgccagatcgccatcgcggccatggtg
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Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
                                                                                    Haemophilus influenzae complete genome sequence
                    AAT42063 standard; DNA; 1830121
                                                                (first entry)
                                                                                                                                                   Haemophilus influenzae
                                          AAT42063;
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Db 230217 gtggcagtttctatcttgatttatatgcacgcgaacacaaacgtggtggtggtggtggtgg 230276 1295 tgggacagttctatttggacctctatccaagggaaggaaaatacaatcatgcggcctgct 1354 g

> W09633276-A1 24-OCT-1996

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the Complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to required the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
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                                                                                                                                                                                                                                                                                                             Haemophilus influenzae Rd genome recorded on computer readable medium - useful for identifying commercially important nucleic acid fragments by homology searching
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                                                                                                                                                                                                           Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 77.2-77.1091; 1291pp; English
                                                                                                                                                                                                        Smith HO,
95US-0487429.
95US-0426787.
95US-0476102.
                                                                                                                 (HUMA-) HUMAN GENOME SCI INC (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                        Fleischmann RD,
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                             21-APR-1995;
07-JUN-1995;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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26-JUL-2000; 2000WO-US20476
                                                    26-JUL-1999; 99US-0145695
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                   gene expression; ss
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                                                The present invention relates to a composition comprising two nucleic
                                                          acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
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                                                                                                                                                                 DB 22; Length 936;
                                                                                                                                                                                        Indels
                                                                                              and single-nucleotide polymorphisms, e.g. for genotyping
                                                                                                                                                                          ilarity 0.8%; Pred. No. 2e-22;
Conservative 475; Mismatches 297;
                                                                                                                                Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other,
                                                                                                                                                                 5.3%; Score 112.8;
0.8%; Pred. No. 2e-2
                         Example 6; Page 127; 159pp; English.
                                                                                                          monitoring gene expression.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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Conservative 475; Mismatches 297; Indels
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                                                                                                                                                                                group; ETM; mismatch; genotyping
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BP
DNA; 936
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                               921 cactgcaaagagcacaaagccgcgtaacagcytttctagatgatttaagccagaagttaaa 980
                                                                                                                                                        gacagaggaactcaagtattccatagaccaagagttcctcaaggaatacttcccaatt 1158
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gene expression; ss.
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17-MAR-2000; 2000US-0190259.
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Seguence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

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   DB 22;
                                                         6; Conservative 475; Mismatches 297;
                                Pred. No. 2e-22;
   5.3%; Score 112.8;
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Query Match
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                                                                                                                    332 atgtatcctctgacaaagaagtacgagcagcaagtacagaagcagacaaaagactttctc 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 127; 159pp; English
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/note= "Ser is O-phosphorylated by CAMP/cGMP-dependent
protein kinase"
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/note= "Ser is O-phosphorylated by protein kinase C"
59..62
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104..107
/note= "Thr is O-phosphorylated by casein kinase II"
114..116
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Human aminopeptidase 22196.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/note= "Thr can be O-phosphorylated by protein kinase C
or by casein kinase II"
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protein kinase"
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protein kinase"
                                                                                          /note="Tyr is O-phosphorylated by a tyrosine kinase"
169..171
/note= "Ser is O-phosphorylated by protein kinase C"
172..175
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518..521
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/note= "Tyr is O-phosphorvlated hw a formand in the contract of 
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242..244
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e= "Thr is O-phosphorylated by casein kinase II"
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543..546
                                                             "Ser is O-phosphorylated by protein kinase C"
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.e- "Thr is O-phosphorylated by protein kinase C"
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/note= "Thr is O-phosphorylated by protein kinase C"
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                   'note= "Ser is O-phosphorylated by casein kinase II"
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.e- "Thr is O-phosphorylated by casein kinase
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te= "Ser is O-phosphorylated by casein kinase
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674..679
/note= "Gly is N-myristoylated"
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.e= "Gly is N-myristoylated"
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:e= "Gly is N-myristoylated"
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This sequence represents a novel human aminopeptidase, designated

22196. CDNA clones encoding human aminopeptidase 22196

were identified in a bone marrow cDNA library using an EST (expressed
cequence tag) selected on the basis of homology to aminopeptidase
cequences, and were assembled to given the full-length cDNA.

Aminopeptidase 22196 is thought to be a metalloenzyme, as it contains
ca zinc-binding region signature found in neutral zinc metallopeptidases.

CC expression analysis indicated that the aminopeptidase is highly
cxpression analysis indicated that the aminopeptidase is highly
cxpression analysis indicated that the aminopeptidase is highly
cxpression analysis indicated that the aminopeptidase is highly
cxpressed in normal osteoblasts, testis, skeletal muscle, foetal kidney
cc expressed in normal breast, lung, and colon
tissue, and is overexpressed in lung and colon cancer. Expression was
cc found to be downregulated during stromal cell osteoblast lineage
cc found to be downregulated during stromal cell osteoblast lineage
cc maturation. Aminopeptidase 22196 may be used to treat pain, and cancers
cc found colon. It can also be used to treat pain, and cancers
cc of the lung and colon. It can also be used to treat pain, and cancers
cc of the used in the treatment of a wide variety of conditions, including
cc splean disorders (e.g., splenomegaly); infectious diseases (e.g.,
ccompounds which bind to it and modulate its activity. Such compounds may
cc malaria, tuberculosis); immune disorders (e.g., rheumatoid arthritis)
cclon disorders (e.g., pulmonary embolism, emphysema, bronchial asthma);
cc liver disorders (e.g., diarrhoea, Crohn's disease, bronchial asthma);
cc of disease, parkinson's disease, Huntington's disease, skin tumours, psorialsis); ardiac and
cvascular disorders (e.g., myocardail infarction, chronic ischemic heart
cc (e.g., vitiligop, urticaria, six disease); and bone disorders (e.g., mayocardail infarction, chronic ischemic etc.
cc steeporosis, paget's disease, Nucleotides encoding aminope
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human aminopeptidose, used to treat colon and lung cancer, and to identify modulators used to treat e.g. cirrhosis \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                             Silos-Santiago I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1A-B; 109pp; English
                                                                                                                                                                                                                                                 White D,
                                                                                                                                                            MILL-) - MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nay be used in gene therapy.
02-OCT-2000; 2000WO-US27214.
                                                                                99US-0409180
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                                                                                                                                                                                                                                                 Kapeller-Libermann R,
                                                                                                                                                                                                                                                                                                                             WPI; 2001-300101/31
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Best Local Similarity
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YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV 480
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                                                                                                                                                                                                                                                                                                                                                                                                                AGRPSLLRHDEVRTYFHEFGHVMHQ1CAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The rabbit endopeptidase was purified from rabbit liver and digested with CNBr. Families of degenerate primers were designed based on the amino acid sequences of the CNBr fragments. The primers were used to amplify sequences from a rabbit cDNA library. An amplified fragment was isolated and used to probe the same library. Two overlapping clones produced a 2148bp sequence. A preliminary sequence analysis was performed in which much of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ಭ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsomal endo-peptidase isolated from rabbit liver cleave protein substrates in=vivo and in=vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabbit endopeptidase (preliminary sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
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N-PSDB; AAQ27307.
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                                                                                                                                                                                                                                            STEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHLP
                                                                                                                                                                                                                                                                                         EQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYKI
                                                                                                                                                                                                                                                                                                                                       TLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' and 3'-most sequences are unassigned; the actual amino and carboxyl terminals of the protein have not yet been determined. The "Others" in the sequence correspond to codons in which I or of the bases has not yet been identified.

See AAR26107-R26113 and AAQ27305-Q27306.
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                                                                                                      Length 709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease; beta amyloid precursor protein; APP; metalloprotease; hAP; protease inhibitor; ss.
                                                                                                                            Indels
                                                                                                     81.2%; Score 2979; DB 13;
86.7%; Pred. No. 2.8e-248;
iive 29; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 AA
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                                                                                                                            Conservative
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                                                                                                      Query Match
Best Local Similarity
Matches 568; Conserv
                                                                     709 AA;
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                                                                      Seguence
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The deduced amino acid sequence of the amyloidin protease contains the motif X +He-E-G-H-X at the active site typical of zinc-dependent metallopeptidases. The enzyme hydrolyses the Met-Asp bond in an amyloid-like substrate, e.g. the bond between Met 596 and Asp 597 of the beta-amyloid core peptide. Inhibitors of amyloidin activity will be potentially useful in therapeutic intervention in Alzheimer's Disease. See also AAR24260-3, AAR24266-7 and AAQ2487-Q24887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVLRWDLSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRY 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKEC 345
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                                    /note= "His residues coordinate Zn2+ ion and Glu is involved in bond-breaking"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like substrate for identifying protease inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 2331; DB 13;
64.9%; Pred. No. 2.3e-192;
Live 98; Mismatches 132;
                                                                                         /note= "immunogenic"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 47-49; 62pp; English
                                                                                                                                                                                                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                     91WO-US07290
                                                                                                                                                                                                                                          90US-0594122
                                                                                                                                                                                                                                                             91US-0766351
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                                                                                                                                                                                                                                                                                                                                                        HF, Johnstone EM,
                   .478
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-167148/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ24875
                                                                                                                                                                                                     04-OCT-1991;
                                                                                                                                                                                                                                                             30-SEP-1991;
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                                                                                                                             WO9207068-A
               Active-site
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Best Local
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                                                                       Peptide
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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide sequences defined in the specification, where the oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprises a 3'-end sequence complementary to a complementary strand of a polynuclectide which comprises a 5'-end sequence (complementary to a polynuclectide which comprises a 3'-end sequence (complementary to a polynuclectide which comprises a 3'-end sequence, where the oligonuclectide comprises a 1'-end sequence (some sequence) and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the specification primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                   645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                               582
                                                                                                                                                                                                                         561
                                                                     501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                  466 MMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFV
                                                                                                                                               EVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVD
                                                                                                                                                                                                                                                                                                                                         QSLHTNTSLDAASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL 701
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Otsuki 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 11797; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:11797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB93028 standard; Protein; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
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the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masignani V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial
                                                                                                                                                                                  06 MNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAMDLYYM 365
                                                                                                                                                                                                                                                                                                     TQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKD 425
                                                                                                                                                                                                                                                   KATGEVLGOFYLDLYPRECKYNHAACFGLOPGCLLPDGSRMMAVAALVVNFSQPVAGRPS 485
                                                                                                                                                                                                                                                                                                                                                                                            SKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCS 605
                                                                                                                                                                                                                                                                                                                                                                                                                                              EILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKY 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRL
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|81 ||thde------tdfarfsgtnvetdfvevpsgmlenwvwdvgslrrl
                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                 Length 381;
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Ratti G, Scarselli M, Scarlato V,
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. gonorrheae amino acid sequence g128.pep SEQ ID NO:53.
                                                                                                                                Score 1981; DB 22;
Pred. No. 1.5e-162;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB58575 standard; Protein; 678
                                                                                                                                54.0%;
95.2%;
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28-FEB-2000; 2000GB-0004695.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) INST GENOMIC RES.
                                                                                                                                                        Matches 380; Conservative
                                                                  of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pizza M, Hickey E,
Galeotti C, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria gonorrheae
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                                                                                                                                              Similarity
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                                                                                            381
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                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB58575;
                                                                                                                                Query Match
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The present invention describes the full length genome of
Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
Lo AAF21613 represent fragments of the NNB genomic sequence, as the
sequence was too long to go in a record on its own it was split into 8
sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
the beginning of AAF21607, the last 49980 bp of AAF21543 repeated at
the beginning of AAF21608, and so on). AAF21545 to AAF21589 to
the beginning of AAF21608, and so on). AAF21545 to AAF21589 to
AAF21606 represent PCR primers which are used in the exemplification of
the present invention. The NNB genome and fragments from it have
antibacterial activity, and can be used in vaccines and gene therapy.
Neisseria nucleic acids, proteins and/or antibodies which binds to the
proteins can be used in compositions for treating or preventing infection
due to Neisserial bacteria or of antibodies raised to Neisserial
bacteria. Computers, computer memory, computer storage medium or computer
catabases can be used in a search to identify open reading frames (ORFS)
or coding sequences within the NNB genome. The DNA sequences: provide
cuther of proteins of the poportunities of the or immunogenic proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                      Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIKTRTEELIVQTKQVYDAVGMLGIEEVT----YENCLQALADVEVKYIVERT-----ML 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shlnsvvdtpelravynelmpeitvffteiggdielynrfktiknspefatlspagktkl 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EREFILNLKKKECKDRGFEYDGKIN--AWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 d-----laevkafarehlgladpqpwdlsyageklreakyafsetevkkyfpvgkvl 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFARFSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLV 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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19.1%; Score 702; DB 21; Length 678;
Best Local Similarity 28.7%; Pred. No. 8.9e-52;
Matches 194; Conservative 127; Mismatches 305; Indels 5
                                                                                                                                                                      Example 1; Page 93-94; 692pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           more effective in vaccines
Grandi G;
                                         2000-647603/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.
                                                                  N-PSDB; AAF21570
Frazer CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes the full length genome of
Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
C to AAF21613 represent fragments of the NMB genomic sequence, as the
sequence was too long to go in a record on its own it was split into 8
sequences which overlap each other at the beginning and end of each
sequences which overlap each other at the beginning and end of each
sequence by 49980 bp (i.e. the last 49980 bp of AAF21607 are repeated at
the beginning of AAF21607, the last 49980 bp of AAF21567 are repeated at
the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
AAF21606 represent PCR primers which are used in the exemplification of
the present invention. The NMB genome and fragments from it have
antibacterial activity, and can be used in vaccines and gene therapy.
Neisserial nucleic acids, proteins and/or antibodies which binds to the
proteins can be used in compositions for treating or preventing infection
due to Neisserial bacteria or as a diagnostic reagent for detecting the
proteins can be used in compositions for treating or preventing the
second of the proteins and proteins and diagnostic reagent for detecting the
proteins can be used in compositions for treating or preventing the
second of the proteins and diagnostic reagent for detecting the
content of the proteins and diagnostic reagent for detecting the
proteins are a diagnostic reagent for detecting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masignani V;
Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial.
                                                                                         Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections - \,
delgvsgingvewdavelpsqfmenfvweynvlagmsaheetgeplpkelfdkmlaaknf 539
                                                       570 NIGLITLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA-TFGHL 625
                                                                                                                                                                     -AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHN 684
                                                                                                                                                                                                       N. meningitidis amino acid sequence m128-1.pep SEQ ID NO:57.
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Scarlato V,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB58577 standard; Protein; 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-1999; 99US-0132068.
08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
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M, Grandi G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB58577;
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AAB58577
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coding sequences within the NMB genome. The DNA sequences provide rther opportunities to find antigenic or immunogenic proteins which are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKSIKMGKRNGLHLPEQVQNEIKSMKRRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 dlaevkafare-sinl-----adlqpwdlgyasekireakyafsetevkkyf 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505 QICAQTDFARFSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKL 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E-----REFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYF 384
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                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                        Score 702; DB 21; Length 678; Pred. No. 8.9e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gonorrheae amino acid sequence g128.pep SEQ ID NO:1013.
                                                                                                                                                                                                                                                   302;
                                                                                                                                                                                                                       Best Local Similarity 28.4%; Pred. No. 8.9e Matches 194; Conservative 126; Mismatches
                                                                                                                                                                                           19.1%; Score 702; 28.4%; Pred. No. 8
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                                                                                                               678 AA
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                                                                                                                  Sequence
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Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserlal infections, for example, N.gonorrhoea -
                                                                               Galeotti
                                                                          Frazer c...,
Masignani V, Galeuc...
     Neisseria gonorrheae.
                                                              (CHIR ) CHIRON CORP.
                                                                                             WPI; 2000-318079/27
                                                                                                    N-PSDB; AAA81285
               WO200022430-A2.
                                    08-OCT-1999;
                                               09-0CT-1998;
                          20-APR-2000
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Scarlato V;

Tettelin H, Venter JC; Ratti G, Scarselli M,

Peterson J, C, Mora M,

98US-0103794. 99WO-US23573

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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414

represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAA825620 to AAA825663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81312 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, artifical proteins of partification of biological probes, artifical production of biological probes, artifical production of biological probes, artifical production of biological probes, artifical productions of biological probes, artificate production of biological probes, artificate production of biological probes, artificate production of biological probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but mone have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.
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Claim 14; Page 93; 1760pp; English.
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Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -

N-PSDB; AAA81287

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Scarlato V;
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                                                                                                                     450
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251 kfdntanidrtlenalktakllgfknyaelslatkmadtpegvlnflhdlarrakpyaek 310
                                                                                               311 d-----laevkafarehlgladpgpwdlsyageklreakyafsetevkkyfpvgkvl 362
                                                                                                                                511 DFARFSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLV 569
                                                                                                                                                                                                                       570 NTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA-TFGHL 625
                                                                                                                                                                                                                                                                -AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHN 684
                                                                                                                                                                                                                                                                                                             --ENTILLQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA
                                                                          EREFILNLKKKECKDRGFEYDGKIN--AWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVT
                                                                                                                     391 EGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAA
                                                                                                                                                                451 CFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitidis amino acid sequence m128-1.pep SEQ ID NO:1017
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M,
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Ratti G, Scarselli
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C, Mora M,
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P. Pizza M;
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30-APR-1999;
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                                                                                       processor specifically claimed Neiseria meningitidis genomic DNA sequences; AAA81260 to AAA8130 and AAB25620 to AAB2563 represent Neiseria DNA sequences and their corresponding processor.

Neiseria DNA sequences and their corresponding processor in the Lands1259 and AAA81254 to AAA81259 and AAA81321 to AAA81259 and AAA81322 to AAA81452 represent Neiseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neiseria meningitidis Menb polyuucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, meningencoccus B vaccines have failed mainly due to antigen tolerance. Whitivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete exposed proteins that may be presumed targets for the immune system and the mark and are not antigened to ratiable or at least more conserved than and the mark of the provision of the mark of the neighbor than and the mark of the provision of the immune system and the mark of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-----REFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYF 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 PIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREG
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19.1%; Score 702; DB 21;
Best Local Similarity 28.4%; Pred. No. 8.9e-52;
Matches 194; Conservative 126; Mismatches 302;
Claim 14; Page 97; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other more variable regions.
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represent novel Neisseria meningitis and N. gonorrheae polynuclectides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynuclectides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. menhagitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynuclectides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
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Scalato E, Scarselli M;
621 -TFGHL-AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDG 678
                                                                                                      AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrheae ORF 128 protein sequence SEQ ID NO:482.
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Ratti G,
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Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                AAY74503 standard; Protein; 678 AA.
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98US-0099062.
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99US-0121528
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98US-0103794
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Tettelin H, Venter JC;
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02-SEP-1998;
02-SEP-1998;
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25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         625
                                                             QIKTRTEELIVQTKQVYDAVGMLGIEEVT---YENCLQALADVEVKYIVERT-----ML 106
                                                                                                      DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166
                                                                                                                       shlnsvvdtpelravynelmpeitvffteiggdielynrfktiknspefatlspagktkl 130
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                                                                                                                                                EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL
                                                                                                                                                                                         PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKE----
                                                                                                                                                                                                                                                                              EREFILNLKKKECKDRGFEYDGKIN--AWDLYYMTQTEELKYSIDQEFLKEYFPIEVVT
                                        50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis ORF 128 protein sequence SEQ ID NO:490
                     Length 678;
                                         Indels
                   19.1%; Score 702; DB 21;
llarity 28.7%; Pred. No. 8.9e-52;
Conservative 127; Mismatches 305;
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                           Local Similarity
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                                        194;
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                    Query Match
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54573 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                         , Mora M;
Scarselli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKSIKMGKRNGLHLPPQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 kfdntanidrtlanalqtakllqfknyaelslatkmadtpeqvlnflhdlarrakpyaek 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 dqiktedikpalqtaiaeareqiaaikaqthtgwantvepltg----itervgriwgvv 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Neisserial polypeptides predicted to be useful antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKE-
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                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V,
Scalato E, S
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                                                                                                                                                                                                                                                                                                                                                                                                      Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                            Galeotti C, Granu. -. -. -. -. -. -. -. -. -. Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 369; 1453pp; English.
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98US-0103796.
99US-0121528.
                                                     98US-0083758.
98US-0094869.
98US-0098994.
98US-0099062.
  99WO-US09346
                                                                                                                                                                       98US-0103749
                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                              Petersen J, Pizza M,
Tettelin H, Venter JC;
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N-PSDB; AAZ53270.
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                                                                                                                                                                       09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
30-APR-1999;
                                                        01-MAY-1998;
                                                                                                                                               02-SEP-1998
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AAY75802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                         563
                                                                                                  VASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA 620
  444
                                      pvgkvlnglfagikklygigftekt-vpvwhkdvryfelgg--ngetiggvymdlyareg 413
                                                                                                                                                                                                                                                                                                                                                        594 lsfghifaggysagyysyawaevlsada-yaafeesddv-aatgkrfwqeilavggsrsa 651
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Scarselli
  PIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREG
                                                                             KYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMH
                                                                                                                                                           505 QICAQTDFARFSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKL
                                                                                                                                                                              -TFGHL-AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDG
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Scalato E, S
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Ratti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 94-95; 1453pp; English.
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Rappuoli
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                                                                                                                                                                                                                                                                                                                                                                                               679 MDMLHNFLKREPNOKAFLMSRG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                   652 aesfkafrgrepsidallrhsg 673
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980S-0098994.
980S-0103749.
980S-0103794.
980S-0103794.
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Petersen J, Pizza M,
Tettelin H, Venter JC;
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N-PSDB; AAZ54602.
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09-0CT-1998;
25-FEB-1999;
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31-JUL-1998;
02-SEP-1998;
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and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 repress pcr primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antipodies, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFARFSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLV 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI----LGVAATPGTNMPA-TFGHL 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 gigtedikpavgt-aiaearggiaavkagthtgwantverltg----itervgriwgvv 70
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                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                         19.1%; .Score 702; DB 21; Length 6; ilarity 28.7%; Pred. No. 8.9e-52; Conservative 127; Mismatches 305; Indels
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Best Local 8
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AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AA52457 to AA254476 and AA524616 to AA255473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                         Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: :| || :| |: :: ::| |::| |: || :: || |: || :: || |: || :: || |: || :: || |: || :: || |: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: 
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16 dqiktedikpalqtaiaeareqiaaikaqthtgwantvepltg----itervgriwgvv 70
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                                                                                        ID NO:3092.
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                                                                               Neisseria meningitidis ORF 128 protein sequence SEQ
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Ratti G,
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Rappuoli R,
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9805-0098994.
9805-0099062.
9805-0103749.
9805-0103794.
                                                                                                                                                                           antigenic; diagnosis; immunc
antibacterial; gene therapy
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                        21-MAR-2000 (first entry)
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Tettelin H, Venter JC;
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                                                                                                                                                                                                                                                                 Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-062150/05.
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09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                        W09957280-A2
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02-SEP-1998;
02-SEP-1998;
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Masignani V;
Rappuoli R;
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                                                                                                                                                     504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|:: |: || | |- |: |
534 laaknfgrgmflvrgmefalfdmmiyseddegrlknwqqvldsvrkkvavigppeynrfa 593
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                                                                                                                   --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA
                                        PIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREG
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PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKE-
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Scarlato V,
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Ratti G, Scarselli M,
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08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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N-PSDB; AAF21571.
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The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 (Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into B caquences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21808 encode the consistent proteins given in AAB58550 to AAB58593, and AAF21589 to the present proteins given in AAB58550 to AAB58593, and AAF21589 to antibacterial activity, and can be used in vaccines and gene therapy. The present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. The present invention of the proteins can be used in compositions for treating or preventing infection cause to Neisserial bacteria or as a diagnostic reagent for detecting the present of Maisserial and the mannifer man bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections - $\,$ Example 1; Page 96; 692pp; English. more effective in vaccines

Seguence

18; 71 shlnsvtdtpelraaynelmpeitvffteiggdielynrfktiknspefdtlshagktkl 130 LLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACF 452 ': | || : | || : | || || 422 dykgrrrfsdglqlptaylvcnftppvggkearlshdeiltlfhetghglhhiltgvde 481 482 lgysgingvewdavelpsqfmenfvweynvlagmsaheetgyplpkelfdkmlaaknfgr 541 GULTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA-TFGHL-A 626 55 EQİKTRTEELIVQT -- KQVYDAVGMLGIEEVT-YENCLQALADVEVKYIVERT-----ML 106 107 DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166 EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223 --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA 332 333 EREFILNLKKKECKDRGFEYDGKINAWDLYYMTQTEELKYSIDQEFLKEYFPIEVVTEG 392 lfaqikklygigftekt-vpvwhkdvryfelqq--ngetiggvymdlyaregkrggawmn 421 Gaps 16 dqiktedikpalqtalaeareqiaalkaqthtgwantvepltg----itervgriwgvv 70 131 nhdlrdfvlsgaelppeqqaelaklqtegaqlsakfsqnvldatdafgiyfddaaplagi 224 PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKE----453 GLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDF 513 ARFSGTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNT 44; Length 678; Indels 18.9%; Score 694; DB 21; ilarity 28.2%; Pred. No. 4.4e-51; Conservative 131; Mismatches 309; Local Similarity Matches 190; Query Match 167 393 365 311 ò g g δλ g g g δ g δ δ g δ δ g à à

nore effective in vaccines

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Sequence

The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21680 encode the Neisseria proteins given in AAB58550 to AAB5859, and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria mucleic acids, proteins and/or antibodies which binds to the proteins and proteins and/or antibodies which binds to the proteins and proteins and/or antibodies which binds to the proteins and proteins and/or antibodies which binds to the proteins and proteins and/or antibodies which binds to the proteins and proteins and/or antibodies which binds to the proteins and proteins and/or antibodies which proteins and proteins and/or antibodies which are used to the proteins and proteins and/or antibodies which binds to the proteins and proteins and/or antibodies which are used antibodies which are used to the proteins and proteins an proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria or of antibodies raised to Neisserial bacteria or of antibodies raised to Neisserial databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are Masignani V. Rappuoli R; Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial. Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections -GGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFL 686 N. meningitidis amino acid sequence a128-1.pep SEQ ID NO:61 Venter JC, Scarlato V, Peterson J, Tettelin H, Ratti G, Scarselli M, Example 1; Page 100-101; 692pp; English. AAB58579 standard; Protein; 678 AA 08-MAR-2000; 2000WO-US05928 2000GB-0004695 (CHIR) CHIRON CORP. (GENO-) INST GENOMIC RES. (first entry) 660 grepsidallrhsg 673 687 KREPNOKAFLMSRG 700 Neisseria meningitidis. Pizza M, Hickey E, Galeotti C, Mora M, Frazer CM, Grandi G; WPI; 2000-647603/62. N-PSDB; AAF21574 WO200066791-A1 08-OCT-1999; 28-FEB-2000; 13-MAR-2001 30-APR-1999; 09-NOV-2000. Frazer CM, AAB58579; RESULT 14 627 AAB58579 셤 δŽ d ò

20-APR-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRREMAFNTRCKE----
                                                                   44;
   Length 678;
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                                                                Indels
18.9%; Score 694; DB 21;
llarity 28.2%; Pred. No. 4.4e-51;
Conservative 131; Mismatches 309;
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414

CC represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent C sequences; AAA81260 to AAA81212 represent PCR primers used in the solution of Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition and antibodies consolved the adentification of the conformation of the conformation of the dentification of the present of a composition and the proteins could be components of vaccines against Meningococcus B; against all serotypes; from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious for control of provision of further, complete conscrome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than conserved than and the conserved th
                                                                                                                                                                                                                                   Scarlato V;
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                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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                                                                                                                                                                                                            Tettelin H, Venter JC;
Ratti G, Scarselli M,
                                                                                                                                                                                                            ckey E, Peterson J,
Galeotti C, Mora M,
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                                         99WO-US23573.
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Neisseria meningitidis Meningococcus B; MenB.

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KDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEG		fareslgladlqpwdlgyageklreakyafsetevkkyfpvgkvlng
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⁶²⁷ GGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFL 686

⁶⁸⁷ KREPNOKAFLMSRG 700 |||: | | | 660 grepsidallrhsg 673 ò

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US-08-647-655-2 US-07-745-206A-1 US-08-311-363-1 Appli , Appl Appli

Sequence 1, A Sequence 23, Sequence 1, A Sequence 1, A

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               Compugen Ltd.
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US-08-231-13
US-08-059-032-13
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Maximum DB seq length: 200000000
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Match 1
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                                                                                                           Perfect score:
                                                                                                                                       Scoring table:
                                            OM nucleic
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st Local Similarity 87.2%; Pred. No. 0;	atches 1728; Conservative 1; Mismatches 247; Indels 6; Ga 1 atjategeceggtgeettttggetgtgegaageeteegeagsttggtggtteeaggatt 	167 ATNATCGCCCGGTGCTTTTCGGCTGTNCGAGGCTCCACAGGGTTGGTGGTTCCAGGATT 22. 61 ttactcagaatgacgttaggaagaagtgatgtctcctctcaggcaatgtcttcctat 12.	227 CTATTCAAAATGACATTAGGAAGAGAGAGATGTCACCTCTTCAGGCAGTTTCTT 121 actgtggctggcagaaatgttttaagatgggatctttcaccagagcaaattaaas 111	28/ ACTGCAGCTGGCAGGAATGTTTAAGATGGGATCTTTCACCAGACCAAATCAGAAGA 34/ 181 actgaggagctcattgtgcagaccaaacaggtgtacgatgccgttggaatgccggtatt 24/ 181 actgaggagctcattgtfgcagaccaaacaggtgtacgatgccgttggaatgccggtatt 24/ 24/ Actacacacacacacacacacacacacacacacacacaca	347 Acjoadogactractacacacacacacacacacacacacacacacaca	40/ ANGGARGIGACITACGAGAACIGCITGCAGGCCCIGGCAGAGIGTGGAGGGAGGTAAAA 40/ ANGGAGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	Angelmeacillectrascatollictrolganacascascascas 22 gcagacaaaagactttctcgttttgatattgagatgagcatgagagga 42 in	421 gatatttgagagaattgttcatttacaggaaacctgtgatctggggaagataaaacct 48	481 gaggccagacgatacttggaaaagtcaattaaaatggggaaaagaaatgggctccatctt 54	catectantestrationnations and categories and catego	/0/ CCNNNNAGAGIACAGATIGANNICAGICAGICAGAGAAGANAANAAAAAAAAAAAAA	601 ggtgotcttcctgatgatttcattgacagtttagaaagacagatgatgacaagtataaa 72	721 attaccttaaatatccacactatttccctgtcatgaagaatgttgtatcct 	781 agagaagatggaaatggcttttaatacaaggtgcaaagaggaaaacaccataattttg 84	841 cagostactcocactgogaaccaaggtggccaaactactcggttatagcacacatgct 9	Qy 901 gacttcgtccttgaaatgaacactgcaaagagcacaagccgcgtaacagcytttctagat 960 	Qy 961 ga [†] tttaagccagaagttaaaaccttgggtgaagcagaacgagagtttattttgaatttg 1020 	Oy 1021 aagaaaaaggaatgcaaagacaggggttttgaatatgatgggaaaatcaatgcctgggat 1080

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APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: McConloque, Lisa C.
APPLICANT: Little, Sheila P.
APPLICANT: Johnstone, Edward M.
APPLICANT: JOHNSTONES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 790.8; DB 1;
Pred. No. 7.3e-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches 743;
                                                                                                                                                           ADDRESSEE: Athena Neurosciences, Inc. STREET: 800F Gateway Blvd. CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/766,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORREY AGENT INFORMATION:
NAME: Murphy, Lisabeth Feix
REGISTRATION UNMBER: 31547
REPERENCE/DOCKET NUMBER: 17796
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 877-8370
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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62.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                          94080
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE:
US-07-766-351-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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            336 ACAAGAACCTGAACGAGGACACGACCTTCCTGCCCTTCACGCTCCAGGAGCTAGGAGGGC
                                                                                                                             TCCCCGAGGACTTTCTGAACTCCCTGGAGAAGATGGAGGACGGCAAGTTGAAGGTCACCC
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                                                 acaaaaacctcaatgaggatgataccttccttgtattttccaaggctgaacttggtgctc
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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                                                                     ; HYPOTHETICAL: N; ANTI-SENSE: NO US-08-059-032-6
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Matches 1236;
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 gaagattgtcaaaaacattataaagatggaagccctattgcagacgatctgcttgaaaaac 1687
                                                                                                                                           aagttgatcagtctcttcataccaacacatcgctggatgctgcaagtgaatatgccaaat 1807
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APPLICANT: Study
APPLICANT: Study
APPLICANT: Dovey, Harry F.
APPLICANT: Dovey, Harry F.
APPLICANT: Dovey, Harry F.
APPLICANT: MCCONLOQUE, Lisa C.
APPLICANT: Little Shella P.
APPLICANT: Callifornia
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/059,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SMILL, WILLIAM E.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/08059032; Patent No. 5424205
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ZIP: 94105
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-059-032-6
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                                                                       128 ctggcagaaatgttttaagatgggatctttcaccagagcaaattaaaacaagaactgagg 187
                                                                                           agctcattgtgcagaccaaacaggtgtacgatgctgttggaatgctcggtattgaggaag
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 Length 2070;
37.4%; Score 790.8; DB 1;
62.4%; Pred. No. 7.3e-217;
live 1; Mismatches 743;
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RESULT 4
PCT-US91-07290-6
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                                                                                                         actacatgactcagacagaggaactcaagtattccatagaccaagagttcctcaaggaat 1147
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CURRENT APPLICATION DATA:
CAPLICATION NUMBER: PCT/US91/07290
FILING DATE: 19911004
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                         APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: McConloque, Lisa C.
APPLICANT: Johnstone, Edward M.
TITLE OF INVENTION: Amyloidin Protease and
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Athena Neurosciences, Inc.
STREET: 800F Gateway Blvd.
CITY: South San Francisco
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 6, Application PC/TUS9107290 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1779
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 877-6900
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murphy, Lisabeth Feix
REGISTRATION NUMBER: 31547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 2070 base pairs NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.4
Best Local Similarity 62.4
Matches 1236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE: NO PCT-US91-07290-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                              94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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g	356	ACCAGAGGATCGTGTGGCTCCAGGAGAAAGTTCAGAAGGACTCACTGAGGCCCGAGGCTG 415	
Øγ	488		i c
QQ	416	CGGGGTACCTGGAGCGGCTAATCAAGCTGGGCCGGAGAAATGGGCTTCACCTCCCCAGAG 475	9 :
δλ	548	aagtacagaatgaaatcaaatcaatgaagaaagaatgagtgag	χ. α.
g	476		1 -
QY Db	536	acaaaaacctcaatgaggatgataccttccttgtattttccaaggctgaacttggtgctc 667 	. do
à	668	ttcctgatgatttcattgacagtttagaaagacagatgatgacaagtataaaattact 72	Oy 1
Q	296	TCCCCGAGGACTITCTGAACTCCCTGGAGAAGATGGAGGACGGCAAGTTGAAGGTCACCC	Qy 1
og Og	656	taaaatatccacactatttccctgtcatgaagaaatgttgtatccctgaaaccagaagaa 787 	Db 1
oy Db	788	ggàtggaaatggcttttaatacaaggtgcaaagagaaaacaccataattttgcagcagc 847 	Qy 1 Db 1
کم ج	848	tacteceactgcgaaccaaggtggccaaactactcggttatagcacacatgctgacttcg 90	0y 1
3 8	0 0	16616ACGC1GCGGGCCCAGAMG1CCCGCC1GCTGGGGTTCCACACGCACGCCGACTATG	0y 1
g G	836	Control of the Cont	
δλ	968	gccagaagttaataccttgggtgaagcagaacgagagtttattttgaatttgaagaaa 10	Qy 2 Db 1
qq	896		
Qy Dp	1028	aggaatgcaaagacaggggttttgaatatgatgggaaaatcaatgcctgggatctatatt 1087 	RESULT US-08-
ογ	1088	actacatgactcagacagaggaactcaagtattccatagaccaagagttcctcaaggaat 1147 	; GEN
QQ	1016		
Qy Dp	1148	actrccaattgaggtggtcactgaaggcttgctgaacacctaccaggagttgttgggac 1207 	
δy	1208	tttcatttgaacaaatgacagatgctcatgtttggaacaagagtgttacactttatactg 1267	« + +
QQ	1136		+ Z C
QY Db	1268	tgaaggataaagctacaggagaagtattggacagttctatttggacctctatccaaggg 1327 	
Qÿ	1328	a aggaaaatacaatcatgggctgcttcggtctccagcctggctgcttctgcctgatg 13	
QQ	1256	AAGGAAAGTACGGCACGCGCCTGCTTTGGCCTGCAGCCCGGCTGCCTGC	
0y	1388	gaageeggatgatggeagtggetgeetegtggtgaaetteteacagecagtggcaggte 144	
g	1316	GGAGCCGCCAGATCGCCGTCGCGGCCATGGTGGCCAACTTCACCAAGCCCACAGCCGACG	
Qy Db	1448	gtöcteteteetgagacaegaegaggtgaggaettaettteatgagtttggteaegtga 1507 	
λ	1508	tgatcagatttgtgcacagactgattttgcacgatttagcggaacaaatgtggaaactg	
ор	1436		; B

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1615
                      1688 ttgttgcttctaggctggtcaacacaggtcttctgaccctgcgccagattgttttgagca 1747
                                                                                                                                                                                                                                                                                      1748 aagttgatcagtetetteataceaacacategetggatgetgeaagtgaatatgeeaaat 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1988 igaaatacagaaacctaatccigaaaccigggggatciciggacggcaiggacaigcicc 2047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2048 acaatttcttgaaacgtgagccaaaccaaaagcgttcctaatgagtagaggcctgcatg 2107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1568 actttgtagaggtgccatcgcaaatgcttgaaaattgggtgtgggacgtcgattccctcc 1627
                                                                                      1628 gaagattgtcaaaacattataaagatggaagccctattgcagacgatctgcttgaaaaac 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1928 ccatggatatgttttacagctgttttaaaaaaagaagggataatgaatccagaggttggaa 1987
                                                                                                               APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Monh. Christine
APPLICANT: Monh. Christine
APPLICANT: Monbland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Respischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
UNMER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uence 839, Application US/08998416
ent No. 6239264
NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27709
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-998-416-839
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APPLICANT: SCHEIFLINGER, F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1609 tgggacgtcgattccctccgaagattgtcaaaacattataaaagatggaagccctattgca 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gacgatctgcttgaaaaacttgttgcttctaggctggtcaacacaggtcttctgaccctg 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1845 cacaaatatgccagcta----cctttggacatttggcagggggatacgatggccaatat 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1372 tgccttctgcctgatggaagccggatgatggcagtggctgcctcgtggtgaacttctca 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1785 tgctgcaagtgaatatgccaaatactgctcagaaatattaggagttgcagctactccagg 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1312 gacctctatccaagggaaggaaatacaatcatgcggcctgcttcggtctccagcctggc 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1432 cagccagiggcaggicgiccitciccigagacacgacgaggigaggactiaciticai 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1492 gagtttggtcacgtgatgcatcagatttgtgcacagactgattttgcacgatttagcgga 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1729 cgccagattgttttgagcaaagttgatcagtctttcatacc----aacacatcgctgga 1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AAGCCGACACCTACCAGACCTGCTCTTCTGAAGTTGGGAGAACTCACAACGTTCTTTCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 CCTGGGTCTGTCCATGGGATTTCGTCGAGGCGCCCTCTCAGATGCTGGAATACTGGACG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GCACGGCGTGACGTTTTAACTATGTTATCCAAGCACTACGAGACAGGTGAGAAAATCCCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AAGTCGCTGCTGGTTTAGTGTTGGCGGCCTCAATTCAGGATTGGCCAACTTG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 GGCCAACTGGAAACTTGGCTTGTTCGACATGTATGTGCACACCCGCGATTACAAAGGAGCG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 GAGGTACGGAAATTATGGAATGATCTCCCCAGAGAGATCGGGCTCATGAACTTAAAAAAC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TACCGTAAGAGAGATGGCTCCAAATCATACCCAGTTACTATCCTTGTGACTAAACTTTTCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1900 tatggatatctttggagtgaagtattttccatggatatgttttacagctgttttaa 1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 TACACTAGCACCGGCTATGACTCCTTTGGACATATTATGGCTGGATATGCTGGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 322; Indels
                                                      PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.1%; Score 86.8; DB 4;
Best Local Similarity 49.1%; Pred. No. 2.5e-15;
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                      TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 322; Conservative
                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: PAG1531RP
US-08-998-416-839
                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                 TOPOLOGY:
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RESULT 6
US-08-232-463-14/C
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.

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211 gtgtacgatgctgttggaatgctcggtattgaggaagtaacttacgagaactgtctgcag 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 gatettteaccagageaaattaaaacaagaaetgaggageteattgtgeagaeeaaaeag 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcactggcagatgtagaagtaaagtatatagtggaaaggaccatgctagactttccccag 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaaacctgtgatctggggaagataaaacctgaggccagacgatacttggaaaagtcaatt 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 cgttttgatattgagatgagcatgagagagagatatatttgagagaattgttcatttacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.9%; Score 61; DB 1; Length 7218;
4.7%; Pred. No. 2e-07;
ive 229; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaaatggggaaaagaaatgggctccatcttcctgaacaagtacagaa 557
                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
FALKNER, F. G.
FENTION: RECOMBINANT FOWLPOX VIRUS
SQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                       COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.78; 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29,768
                                                                       E: Foley & Lardner
1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 4.7% Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                      DATA:
               TITLE OF INVENTION: REVUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                           STREET: 1800 Dia CITY: Alexandria
                                                                                                                                               COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                         ADDRESSEE:
                                                                                                                                ΚX
                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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1085 RRRRRRRRRRRRRRRRRRRRRRRR 1039
                                                                                                                                                                                                              APPLICANT: Sinha, Sukanto
APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry P.
APPLICANT: Dovey, Harry P.
APPLICANT: Little, Sheila P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Johnstone, Edward M.
APPLICANT: Johnstone, Application Protease and Uses Thereof NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERAȚING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1;
Pred. No. 0.0055;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATCOREX/AGENT INFORMATION:
NAME: MAIPHY, Lisabeth Feix
REGISTRATION NUMBER: 31547
REFERENCE/DOCKET NUMBER: 17796-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEPHONE: (415) 877-8370
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Athena Neurosciences, Inc. STREET: 800F Gateway Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08059032; Patent No. 5424205; GENERAL INFORMATION: APPLICANT: Sinha, Sukanto APPLICANT: Seubert, Peter A. APPLICANT: Dovey, Harry F.
                                                                                                                                        Sequence 13, Application US/07766351
Patent No. 5292652
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.0%;
Best Local Similarity 73.0%;
Matches 54; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
LENGTH: 75 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: | nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTGGGCCTGGCCTT 74
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US-07-766-351-13
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1141 aaggaatacttcccaattgaggtggtcactgaaggcttgctgaacacctaccaggagttg 1200
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Pred. No. 0.0055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sinha, Sukanto
APPLICANT: Seubert, Peter A.
APPLICANT: Seubert, Peter A.
APPLICANT: McConloque, Lisa C.
APPLICANT: Johnstone, Edward M.
APPLICANT: Johnstone, Edward M.
ATTLE OF INVENTION: Amyloidin Protease and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Athena Neurosciences, Inc.
                 APPLICANT: Little, Sheila P.
APPLICANT: Johnstone, Edward M.
AITLE OF INVENTION: Amyloidin Protease and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
CARRESPONDENCE TOWNSEND and Townsend Khourie and Crew
STREET: One Market plaza, Steuart Street Tower,
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDUTER READABLE FORM:
MEDUTER READABLE FORM:
MEDUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/059,032
FILING DATE: 19930507
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, William E.
REGISTRATION NUMBER: 15270-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 326-2400
TELEPRAX: (415) 326-2400
TELERAX: (415) 326-2400
TELERAX: (415) 326-2400
TELERAX: (55 300 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TURDENGRATION FOR SQUENCE
LENGTH: 75 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application PC/TUS9107290 GENERAL INFORMATION:
McConlogue, Lisa C.
Little, Sheila P.
Johnstone, Edward M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.0%
Best Local Similarity 73.0%
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                          CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CTGGGCCTGGCCTT 74
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PCT-US91-07290-13
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LENGTH: 164 base pairs
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: 1
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Patent No. 5292652

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Subbert, Peter A.
APPLICANT: McConloque, Lisa C.
APPLICANT: Intite, Sheila P.
APPLICANT: Intite, Sheila P.
APPLICANT: Johnstone, Edward M.
TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 42; DB 5; Length 75; 73.0%; Pred. No. 0.0055;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,351
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OCREVER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07290
FILLING DATE: 19911004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                 17796-002
                                                                                                                                                                                CLASSIFICATION:
NAME: MUTDHY, LISADECH FEIX
REGISTRATION NUMBER: 31547
REGISTRATION NUMBER: 31547
REFERENCE/DOCKET NUMBER: 117796
TELEPHONE: (415) 877-0900
TELEFHORE: (415) 877-0900
TELEFAX: (415) 877-0900
TELEFAX: (415) 877-0370
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Lisabeth Feix
REGISTRATION NUMBER: 31547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 800F Gateway Blvd.
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 73.0
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1201 ttgggactttcatt 1214
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11near
MOLECULE TYPE: CDNA
                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-07-766-351-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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775 gaaaccagaaggaaggatggaaatggcttttaatacaaggtgcaaagaggaaaacaccata 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 GGAAAGTGGAGGGCTTCAACTGCCGGTGCAAGCCGGTGCAAGGAGGAGAAACTGCGCT 85
                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 164;
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Pred. No. 0.012;
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APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: Little, Shella P.
APPLICANT: Little, Shella P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Johnstone, Edward M.
ANTILE OF INVENTION: Amyloidin Protease and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Market Plaza, Steuart Street Tower, STREET: Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.0%; Score 41.4; DE Best Local Similarity 56.1%; Pred. No. 0.012 Matches 78; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/059,032
FILING DATE: 19930507
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Smith, William E.
REGIGSRATION NUMBER: 30,223
REFERENCE/CDCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
             TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          895 catgctgacttcgtccttg 913
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                                                                                                                          LENGTH: 164 base pairs TYPE: nucleic acid
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Sequence 23, Application US/09056105 Patent No. 6287569
2.08;
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Best Local Similarity 55.0
Matches 71; Conservative
                                     Conservative
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US-09-056-105-23
Query Match
Best Local Similarity
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US-09-056-105-23/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 23
LENGTH: 1821
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                                     Matches
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                                                                                                                                                                                                                                                                                                              835 attittgcagcagctactcccactgcgaaccaaggtggccaaactactcggttatagcaca 894
                                                                                                                                                                                                                                                                          26 GGAAAGTGGAGGAGGCCTTCAACTGCCGGTGCAAGCCGGTGCAAGGAGGAGAACTGCGCT 85
                                                                                                                                                                                                         ;
0
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APPLICANT: Subbert, Peter A.
APPLICANT: McConlogue, Lisa C.
APPLICANT: Little, Sheila P.
APPLICANT: Little, Sheila P.
APPLICANT: Little, Sheila P.
APPLICANT: TITLE OF INVENTION: Amyloidin Protease and Uses Thereof NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                       Indels
                                                                                                                                                                 Score 41.4; DB 1; I Pred. No. 0.012; 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Athena Neurosciences, Inc. 800F Gateway Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Murphy, Lisabeth Feix
REGISTRATION NUMBER: 31547
REFERENCE/DOCKET NUMBER: 17796-002
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (415) 877-0900
TELEFAX: (415) 877-0900
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US91/07290
FILING DATE: 19911004
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application PC/TUS9107290 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 800F Galery, STREET: 800F Galery, South San Francisco GTATE: California
                                                                                                                                                                   2.0%;
56.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                            146 CACGCCGACTATGTCCTGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 164 base pairs
TYPE:| NUCLEIC ACID
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
     nucleic acid
                                                                                                                                                                                    Local Similarity
nes 78; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                        MOLECULE TYPE: CDNA
                                   linear
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                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: | 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
PCT-US91-07290-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12 | PCT-US91-07290-16
                                                                                            ANTI-SENSE:
                                                                                                              US-08-059-032-16
                                                                                                                                                                   Query Match
Best Local
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                                                                                      775 gaaaccagaagaaggatggaaatggcttttaatacaaggtgcaaagggaaaacaccata 834
                                                                                                                                                                         835 attitigcagcagctactcccactgcgaaccaaggtggccaaactactcggttatagcaca 894
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US-08-253-503-1/c
Sequence 1, Application US/08253503
Sequence 1, Application US/08253503
GENERAL INFORMATION:
APPLICANT: Coulte, Pierre
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: FOR A TUMOR REJECTION ANTIGEN PRECURSOR
TITLE OF INVENTION: WHICH IS PROCESSED TO AN ANTIGEN PRESENTED
TITLE OF INVENTION:
BY HLA-B44, AND USES THEREOF
                                                                                                                               26 GGAAAGTGGAGGAGGCCTTCAACTGCCGGTGCAAGCCGGTGCAAGGAGGAGAACTGCGCT
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Pred. No. 1.3;
0; Mismatches 58; Indels 0
    Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
APPLICANT: WINDI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/211
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
Score 41.4; DB 5; Length 1
Pred. No. 0.012;
0; Mismatches 61; Indels
                                              0; Mismatches
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: 805 Third Avenue
New York
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CITY: Ne
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Pred. No. 1.3;
0; Mismatches 58; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Herman, Jean; Coulie, Pierre;
APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
APPLICANT: Luescher, Immanuel.
TITLE OF INVENTION: Tumor Rejection Antigens Presented By
TITLE OF INVENTION: HAA-B44 Molecules, And Uses Thereof
COUNTRY: USA
2.DF: 10022
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,503
FILING DATE: June 3, 1994
CLASSIFICATION: 435
ATTORNEY ACCOUNT.
                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LUD 5378
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARATERIES:
LENGTH: 1896 base pairs
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,883
FILLING DATE: 06-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5589334man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,506
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Patent No. 5744353
GENERAL INFORMATION:
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STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
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US-08-796-883-1/c
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FILING DATE: 20-FEBRUARY-1996
FILING DATE: 12-SEPEMBER-1935
FRICA PAPTICATION NUMBER: 08/531,864
FILING DATE: 12-SEPEMBER-1935
FRICA APPLICATION NUMBER: 08/373,636
FILING DATE: 17-TANDARY-1995
FRICA RAPLICATION NUMBER: 08/273,636
FILING DATE: 3-JUNE-1944
FILING DATE: 3-J
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N. A

us-09-833-782-2.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 14, 2002, 18:56:36; Search time 63.23 Seconds (without alignments) 408.225 Million cell updates/sec

US-09-833-782-2 3668 1 MIARCLLAVRSLRRVGGSRI......FLKREPNQKAFLMSRGLHAP 704 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	002038 sus scrofa P42676 rattus norv P42678 sus scrofa P5288 homo sapien P52188 saccharomy P25375 saccharomy P27237 salmonella Q99737 homo sapien P27237 salmonella Q99737 homo sapien P27236 salmonella Q99797 homo sapien Q01992 rattus norv P35999 saccharomy Q10192 rattus norv P35999 saccharomy Q10415 schizophyll Q9996 h a kinase O51264 borrealia bu Q58445 methanococc Q62209 mus musculu P30622 homo sapien Q94822 homo sapien Q94832 homo sapien Q364846 saccharomyc G5840 sus scrofa Q28628 oryctolagus Q03410 rattus norv P94876 lactococcus
SUMMARIES	NEUL_RABIT MEUL_RABIT MEUL_RABIT MEDD_HUMAN MEPD_HUMAN MEPD_HUMAN MEPD_RAT PRID YEAST OPDA_ECOLI OPDA_ABITY OPDA_BALTY PMIP_HUMAN OPDA_BALTY PMIP_RAT PMIP_RAT PMIP_RAT PMIP_RAT PMIP_SCHCO PMIP_SCHCO PMIP_SCHCO PMIP_SCHCO PMIP_SCHCO MIP_SCHCO MIP_
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Result No.	10000000000000000000000000000000000000

		Q01397 neurospora									
MYH9_HUMAN	CENF_HUMAN	DYNA_NEUCR	MYS2_SCHPO	LMG1_HUMAN	GOG4_HUMAN	MYSB_CAEEL	MYHB_RABIT	NUF1_YEAST	RYNR_HUMAN	ANX6_BOVIN	T2BR_BACSU
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ALIGNMENTS

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rissum=Liver;
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P42675;
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                                                                                                            NEUROLYSIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
A02BFEC67B7044A1 CRC64;
                                                                                                                                                                      Length 704;
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                                                                                                                                                                                      15; Mismatches
               JOINED.
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                                                                  InterPro; IPR001567; Peptidase_M3. InterPro; IPR000130; Zn_MTpeptdse.
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EMBL; AB000418; BAA19104.1; JC
EMBL; AB000419; BAA19104.1; JC
EMBL; AB000420; BAA19104.1; JC
EMBL; AB000421; BAA19104.1; JC
EMBL; AB000422; BAA19104.1; JC
EMBL; AB000424; BAA19104.1; JC
EMBL; AB000424; BAA19104.1; JC
FIR; A43411; A43411.
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawabata S.-I., Nakagawa K., Muta T., Iwanaga S., Davie E.W.;
"Rabbit liver microsomal endopeptidase with substrate specificity
processing proproteins is structurally related to rat testes
metalloendopeptidase 24.15.",
J. Biol. Chem. 268:12498-12503(1993).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last ennotation update)
NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE)
(MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP)
                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ALB/F4DE38E8088C CRC64;
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Metalloprotease; Hydrolase; Zinc; Mitochondrion; Transit pr
TRANSIT 37 MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Euthería; Lagomorpha; Leporidae; Oryctolagus.
661 VGMKYRNLILKPGGSLDGMDMLQNFLKREPNQKAFLMSRGLHAP 704
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InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROLYSIN ENDOPEPTIDASE)
(MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).
Rattus norvegicus (Rat).
ITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
                                                                                                                                            LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
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                                                                                         DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
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-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INTERMEMBRANE SPACE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serizawa A., Dando P.M., Barrett A.J.;
"Characterization of a micochondrial metallopeptidase reveals neurolysin as a homologue of thimet oligopeptidase.";
neurolysin as a homologue of thimet oligopeptidase.";
J. Biol. Chem. 270:2092-2098(1995).
-!- FUNCTION: HYDROLYSES OLIGOPEPTIDES SUCH AS NEUROTENSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRADYKININ, DYNORPHIN A, ETC.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE IN NEUROTENSIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain; MEDLINE=96070836; PubMed-7592986; Dauch P., Vincent J.-P., Checler F.; Molecular cloning and expression of 3.4.24.16." J. Biol. Chem. 270:27266-27271(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95138171; PubMed=7836437;
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REMBL; X87157; CAA60630.1,

REMBL; X87157; CAA60630.1,

REMBL; X87157; CAA60630.1,

RICHEPTO: IPRO0130; Zn_MTBPETGSe.

DR Pfam; PF001432; Peptidase_M3: 1.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

KW Metalloprotease; Hydrolase; Zinc, Mitochondrion; Transit peptide.

FT TRANSIT 38 704 MITOCHONDRION.

FT ACT_SITE 498 498 BY SIMILARITY:

ACT_SITE 498 498 BY SIMILARITY:

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ACT_SITE 677 497 2INC (CATALYTIC) (BY SIMILARITY:

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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC )
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY
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89.7%; Pred. No. 1.8e-199;
ive 40; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- TSSUE SPECIFICITY: UBIQUITOUS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
601 AKYCTEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFHSCFKKEGIMNPE 660
                                                                                                                                                                                                                                                                                         Kato A., Sugiura N., Hagiwara H., Hirose S., "Cloning, amino acid sequence and tissue distribution of porcine thimet oligopeptidase. A comparison with soluble angiotensin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF THE PHE-|-ALA BOND IN SUBSTRATES CONTAINING -PHE-PHE-|-ALA-ALA-PHE- AND SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNDER 20
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Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                   Kato A., Sugiura N., Saruta Y., Hosoiri T., Yasue H., Hirose S. Targeting of endopeptidase 24.16 to different subcellular compartments by alternative promoter usage.";
J. Biol., Chem. 272.15313-15322(1997).
-i. FUNCTION: INVOLVED IN THE METABOLISM OF NEUROPEPTIDES UNDE AMINO ACID RESIDUES LONG: INVOLVED IN CYTOPLASMIC PEPTIDE
                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
THIMET OLIGOPEPTIDASE (EC 3.4.24.15) (ENDOPEPTIDASE 24.15)
                                                                                                                                                                                                           Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                      686 AA
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                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED
                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem. 221:159-165(1994)
                                                                                                                                                                                                                                                                                  MEDLINE-94222057; PubMed-8168506;
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
MEDLINE=97326108; PubMed=9182559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: BINDS ONE ZINC ION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB000438; BAA19107.1;
AB000426; BAA19107.1;
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BAA19107.1;
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BAA19107.1;
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                                                                                                             STANDARD;
                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           FROM N.A.
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AB000430;
                                                                                                                                                                                                 Sus scrofa (Pig)
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AB000433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCES
                                                                                                                                                                                                                                                                       rissum-Liver,
                                                                                                            MEPD_PIG
P47788;
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                                                                                                                                                                                                                                                                                                                                  protein!"
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                                                                                                MEPD_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448
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                                                                                                                                                                                                                                                                                                                                                                                                                          208
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                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      29 EVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENC
                                                                                                                                                                                                                                                                                                             209 DDTFLVFSKAELGALPDDFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 QIDFARFSGINVEIDFVEVPSOMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 LQETCDLGKIKPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 VTEGLINTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNH
                                                                                                                                                                                                                                                      8;
                                                                                                                BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
AA6006223047580C CRC64;
                                                                                BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                   Length 686;
                                                                                                                                                                                                                     Ouery Match 63.5%; Score 2330; DB 1; Best Local Similarity 64.0%; Pred. No. 1.3e-136; Matches 431; Conservative 104; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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                      Pfam, PF01432; Peptidase_M3; 1.
PROSTIE: PS00142: ZINC_PROTEASE; 1.
Metalloprotease; Hydrolase; Zinc.
INIT_MET 0 0 BY SIM
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InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                       78013 MW;
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476
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664 DPKQDAFLLSKGL 676
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MEPD_HUMAN
ID MEPD_HUMAN
AC P52888;
DT 01-0CT-1996 (
DT 01-0CT-1996 (
DT 01-0CT-1996 (
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DFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLP 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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P24155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRY 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Taylor G.R., Otulakowski G., Lau C.Y., Munroe D.G.;

Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: INVOLVED IN THE METRABOLLSW OF NEUROPEPTIDES UNDER 20

AMINO ACID RESIDUES LONG. INVOLVED IN CYTOPLASMIC PEPTIDE
DEGRADATION. ABLE TO DEGRADE THE BETA-AMYLOID PRECURSOR PROTEIN
AND GENERATE AMYLOIDOGENIC FRAGMENTS.

-1- CAPALYTIC ACITVITY: PREFERENTIAL CLEAVAGE OF THE PHE-1-ALA BOND
IN SUBSTRATES CONTAINING -PHE-PHE-1-ALA-ALA-PHE- AND SIMILAR
                                                                                                                                                                        Thompson A., Huber G., Malherbe P., a metalloendopeptidase from "Cloning and functional expression of a metalloendopeptidase from human brain with the ability to cleave a beta-APP substrate
THIMET OLIGOPEPTIDASE (EC 3.4.24.15) (ENDOPEPTIDASE 24.15) (MP78)
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                   Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97; Mismatches 133; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 2330; DB 1;
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                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 213:66-73(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Metalloprotease; Hydrolase; Zinc.
INIT_MET 0 0 BY SIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                           MEDLINE=95367027; PubMed=7639763;
                                                 Chordata;
                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78708 MW;
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                                   Homo sapiens (Human)
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                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M03.001;
MIM; 601117; -.
                                                                                     NCBI_TaxID=9606;
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                                                                                                                                          TISSUE=Brain;
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protein, and some corrections to the published amino acid sequence of the rat testis enzyme.";
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01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
(ENDOPEPTIDASE (BC. 3.4, Last annotation-collicopertidase A)
(ENDOPEPTIDASE 24.15) (PZ-PEPTIDASE) (SOLUBLE METALLO-ENDOPEPTIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pierotti A., Dong K.-W., Glucksman M.J., Orlowski M., Roberts J.L.; "Molecular clothing and primary structure of rat testes metalloendopeptidase EC 3.4.15."; Biochemistry 29:10323-10329(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF THE PHE-|-ALA BOND IN SUBSTRATES CONTAINING -PHE-PHE-|-ALA-ALA-PHE- AND SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. J. 295:57-60(1993).
286 LRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKEC
                                                                                                     346 KDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSF
                                                                                                                                                                                                                   406 EQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSR
                                                                                                                                                                                                                                                                                                                                                                                                     466 MMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             646 MFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL 701
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SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: IS EXPRESSED ABUNDANTLY IN THE TESTIS.
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PRTD_YEAST P25375;
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercial entities, requires a license agreement (See http://www.isb-sib.ch/announce
IT IS ALSO FOUND IN THE LIVER, LUNG AND KIDNEY.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO, KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
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SINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
FSOB6290E0B6EA12 CRC64;
                                                                                                                                                                                                                              ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                    Length 686;
                                                                                                                                                                                                                                                                                                   62.5%; Score 2291; DB 1; Length 664.3%; Pred. No. 3.3e-134;
ive 98; Mismatches 136; Indels
                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                   Pfam; PF01412; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Metalloprotease; Hydrolase; Zinc.
                                                                                                                                                      MEROPS; M03.001; -.
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                          EMBL; M61142; AAA41586.1; -.
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PIR; S38760; S38760.
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486 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94139744; PubMed=8307027;
MEDCLINE=94139744; PubMed=8307027;
Buechler M., Tisljar D., Wolf D.H.;
"Proteinase yscD (oligopeptidase yscD). Structure, function and
relationship of the yeast enzyme with mammalian thimet oligopeptidase
(metalloendopeptidase, EP 24.15).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBGELLUTAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE):
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Voet M., Volckaert G.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: COULD BE INVOLVED IN LATE STAGE OF PROTEIN DEGRADATION.
--- CATALITIC ACTIVITY: CLEAVAGE OF PRO--PHE AND ALA-1-ALA BONDS.
--- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
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646 MFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

340910B7FDAEBE37 CRC64;
                                   Length 712
                                                                                                                                                                                                                                                                                 01-WAY-1992 (Rel. 22, Created)
15-DEC-1998 (Rel. 37, Last annotation update)
SACCHAROLYSIN (EC 3.4.24.37) (PROTEASE D) (PROTEINASE YSCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.6%; Score 1085.5; DB 1; Length Best Local Similarity 35.2%; Pred. No. 9.5e-60; Matches 251; Conservative 130; Mismatches 295; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alexandraki D., Galland P., Thireos G., Tzermia M.; submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                       712
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PRD1 OR YCL057W OR YCL57W.
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                                                                                                                                                                                                                          STANDARD;
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                                                                          FYDS--MSKVESPSVSNFVEPFMKFENELGPIINOLIFLOHVSSDKEIRDASVNSSMKLD 121
                                                                                                                           RFDIEMSMRGDIFERIVH----LOETCDLGKIKPEARRYLEKSIKMGKRNGLHLPEQVQN 186
                                                                                                                                                     EIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDK-----YK 240
                                                                                                                                                                                                                                    241 ITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDAAS--EYAKYCSEILGVAATPGTNMPA--TFGH-LAGGYDGQYYGYLWSEVFSMDMFY 648
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Conlin C.A., Trun N.J., Silhavy T.J., Miller C.G.;
"Escherichia coli prlC encodes an endopeptidase and is homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93374878; PubMed=8366062;
Conlin C.A., Miller C.G.;
"Location of the prIC (opdA) gene on the physical map of Escherichia
LLCKNWFASPVISPLLYTRSLYSMANTTSFPIAPQAPPNWSFTPSDISGKTNEIINNSNN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
OLIGOPEPTIDASE A (EC 3.4.24.70).
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J. Bacteriol. 174:5881-5887(1992)
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SOTIALINE=94316500; PubMed=8041620;

A Sofia H.J. Butland V., Daniels D.L., Plunkett G. III, Blattner F.R.;

"Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";

"Involeic Acids Res. 22:2576-258(1994).

"Involeic Acids Res. 22:2576-2580 FROM PRECURSOR FORMS OF SIGNAL PROTEINS. CAN CLEAVE NACETYL-LALA4.

"EPPTIDES AFTER THEY ARE RELEASED FROM PRECURSOR FORMS OF SECRETED PROTEINS. CAN CLEAVE NACETYL-LALA4.

"CATALYTIC ACTIVITY: HYDROLYSIS OF OLIGOPEPTIDES, WITH BROAD SPECIFICITY. GLY OR ALA COMMONIX OCCUR AS PI OR PI'R FSIDUES, BUT MORE DISTANT RESIDUES ARE ALSO IMPORTANT, AS IS SHOWN BY THE FACT THAT Z-GLY-PRO-GLY-I-GLY-PRO-ALA IS CLEAVED, BUT NOT Z-(GLY)5.

"ITAL Z-GLY-DRO-GLY-I-GLY-PRO-ALA IS CLEAVED, BUT NOT Z-(GLY)5.

"ITAL Z-GLY-DRO-GLY-I-GLY-PRO-ALA IS CLEAVED, BUT NOT Z-(GLY)5.

"ITALIANITY: BELONGS TO PEPTIDASE FAMILY MISCALL METALLOPROTEASE);
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R EMBL; M00039; AAB18474.1; -

R EMBL; ABC00426; AAC76523.1; -

R ENT. A43329; A43329.

R ECGENC; E011441; prlC.

R InterPro; IPR00136; Zn_MTpeptdse.

R InterPro; IPR00136; Zn_MTpeptdse.

R PROSITE; PS00142; ZINC_PROTASE; 1.

R PROSITE; PS00142; ZINC_PROTASE; 1.

R Hydrolase; Metalloprotease; Zinc; Complete proteome.

W Hydrolase; Metalloprotease; Zinc; Carally (BY SIMILARITY).
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ZINC (CATALYTIC) (BY SIMILARITY).
LL -> FV (IN REF. 1).
LR -> AA (IN REF. 1).
D -> H (IN REF. 1).
S -> T (IN REF. 1).
A -> G (IN REF. 1).
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Bacteriol. 175:5731-5732(1993)
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-!- CATALYTIC ACTIVITY: HYDROLYSIS OF OLIGOPEPTIDES, WITH BROAD SPECIFICITY. GLY OR ALA COMMONLY OCCUR AS PI OR PI'RESIDUES, BUT MORE DISTANT RESIDUES ARE ALSO IMPORTANT, AS IS SHOWN BY THE FACT THAT Z-GLY-PRO-GLY-I-GLY-PRO-ALA IS CLEAVED, BUT NOT Z-(GLY)5.

-!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY M3 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
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                               366 TQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKD 425
                                                                                               KATGEVLGQFYLDLYPREGKYNHA---ACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAG 482
                                                                                                                                                                                                                          LRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYA 601
                                                                                                                                                                                                                                                                                            602 KYCSEILG-VAATPGTN----MPATFGHL-AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGI 656
                                                                                                                                                                                                                                                          LAFISGHYETGEPLPKELLDKMLAAKNYQAALFILRQLEFGLFDFRLHAEFRPDQGAKIL 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE—95350630; PubMed=7542800; Relation R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fleids C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fubrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                              339 EKOKOHLYSISDEQLRPYFPENKAVNGLFEVVKRIYGITAKERKDVDVWHPDVRFFELYD
                                                                                                                                                                              RPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSG-TNVETDFVEVPSQMLENWVWDVDS
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
OLIGOPEPTIDASE A (EC 3.4.24.70).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                   Pram: PFO1432: Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Complete proteome.
METAL 470 470 ZINC (CATALYIC) (BY SIMILARITY).
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ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)

1452905A001ECFC5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206; Conservative 127; Mismatches 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 814.5; DB 1
Pred. No. 4.9e-43;
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                                                                                                                                           InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
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30.3%;
EMBL; U32706; AAC21882.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                        MEROPS; M03.004;
                                                                                                  TIGR; HI0214;
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Conlin C.A., Miler C.G.;

Conlin C.A., Miler C.G.;

Cloning and nucleotide sequence of opda, the gene encoding and nucleotide sequence of opda, the gene encoding repetidase A in Salmonella typhimurium.";

Ulgopeptidase A in Salmonella typhimurium.";

I Bacteriol. 174:1631-1640(1992).

-! FUNCTION: MAY PLAY A SPECIFIC ROLE IN THE DEGRADATION OF SIGNAL PEPTIDES AFTER THEY ARE RELEASED FROM PRECURSOR FORMS OF SECRETED PROTEINS. CATALITY: THEY DESCRIPTION OF CIGOPEPTIDES, WITH BROAD SPECIFICITY. GLY OR ALA COMMONLY OCCUR AS PI OR P1' RESIDUES, BUT MORE DISTANT RESIDUES ARE ALSO IMPORTANT, AS IS SHOWN BY THE FACT THAT Z-GLY-PRO-GLY-PRO-ALA IS CLEAVED, BUT NOT Z-(GLX)S.

-! COPACTOR: BINDS ONE ZINC ION.

-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);

C. -! CORNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R Pfam; PF01432; Peptidase_M3; 1.

R PROSTITE; PS00142; ZINC_PROTEASE; 1.

KW Hydrolase; Metalloprotease; ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT_SITE 470 470 BY SIMILARITY.

WETAL 473 473 ZINC (CATALYTIC) (BY SIMILARITY).

476 ZINC (CATALYTIC) (BY SIMILARITY).

ATTAL 476 ZINC (CATALYTIC) (BY SIMILARITY).

ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL ATTAL A
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Pred. No. 1.6e-42;
                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-18
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92165739; PubMed=1537805;
                                                                                            01-NOV-1995 (Rel. 32, Last anno:
OLIGOPEPTIDASE A (EC 3.4.24.70)
                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seq
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30.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: RELEASE OF AN N-TERMINAL OCTAPEPTIDE AS SECOND STAGE OF PROCESSING OF SOME PROTEINS IMPORTED IN THE MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STIMULATED BY MANGANESE, MAGNESIUM OR CALCIUM IONS AND REVERSIBLY INHIBITED BY ZINC, COBALT, AND IRON (BY SIMILARITY).
SUBDNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
253 WDNSPVMEEILALRHELAQLIGFENYAHESLATKMAENPQQVLDFLTDLAKRARPQGEKE 312
                                                                                                                                                                                                                                                                       569
                                                                                                                                                                                                                                                                                                           542
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                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59) (MIP).
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                                                                                                                                                 511 DFARFSG-TNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLV
                                                                                                                                                                                                                                                                                            REFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGL
                                                                                                                           394 LNTYOELLGLSFEOMTDAHVWNKSVTLYTVKDKATGEVLGOFYLDLYPREGKYNHA---A
                                                                                                                                                                                                    CFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQ1CAQT
                                                                                                                                                                                                                                                                                                                                            570 NTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI-LGVAATPGT---NMPATFGHL
                                                                                                                                                                                                                                                                                                                                                                              543 QAALFILRQLEFGLFDFRLHAEFNPQQGAKILETLFEIKKQVAVVPSPTWGRFPHAFSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 40:493-496(1997).
-!- FUNCTION: CLEAVES PROTEINS, IMPORTED INTO THE MITOCHONDRION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chew A., Buck E.A., Peretz S., Sirugo G., Rinaldo P., Isaya G., "Cloning, expression, and chromosomal assignment of the human mitochondrial intermediate peptidase gene (MIPEP).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713 AA.
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MEDLINE=97230465; PubMed=9073519;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Q99797;
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EMBL; X57947; CAA41014.1; -.
EMBL; AE000251; AAC74611.1; -
EMBL; D90796; BAA15228.1; -.
EMBL; D90797; BAA15240.1; -.
PIR; S14870; S14870.
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694 V 694
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                                                                                                                                                                                                                                                                                                              103 OTVLIFDEL-----SDSLCRVAD------LADFVKIAHPEPAFREAAEEAC 142
                                                                                                                                                                                                                                                                                                                                    127 KRLSRFDIEMSMRGDIFERIVHLOETCDL-GKIKPEARRYLEKSIKMGKRNGLHLPEQVQ 185
                                                                                                                                                                                                                                                                                                                                                 229 DSL--EKTDD----DKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKK 342
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                                                                                                                                                                                                                                                                                          67 QTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRAASTEAD 126
                                                                                                                                                                                                                   Best Local Similarity 25.9%; Pred. No. 3.9e-25;
Matches 187; Conservative 112; Mismatches 302; Indels 120; Gaps
                                                                                                                                                                                                                                                  17 GSRILLRMTLGREVMSP-LQAMSSYTVAGRNVLRWDLSPEQIKTRTEELI------V 66
                                                                                                                 MITOCHONDRIAL INTERMEDIATE PEPTIDASE.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
A491FCA95CD84054 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               NEIKSMKKRMSELCIDFN-KNLNEDDTFLVF----SKAELGALPDD------FI
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InterPro: IPR000130; Zn_MTpeptdse.
Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolasse; Metalloprotease; Zinc; Transit peptide; Mitochondrion; Magnesium; Manganese, Calcium; Cobalt; Iron.
TRANSIT 1 35 MITOCHONDRION.
                                                                                                                                                                                                       14.3%; Score 525; DB 1; Length 713; 25.9%; Pred. No. 3.9e-25;
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           EMBL; U80034; AAC51231.1;
MEROPS; M03.006; -.
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713 AA;
                                 MIM; 602241;
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-:- CATALYTIC ACTIVITY: HYDROLYSIS OF UNBLOCKED, C-TERMINAL DIPEPTIDES FROM OLIGOPEPTIDES, WITH BROAD SPECIFICITY. DOES NOT HYDROLYSE BONDS IN WHICH PI'S PRO, OR BOTH PI AND PI'ARE GLY.
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mixi T., Mazobuchi K., Mori H., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takenchi Y., Wada C., Yamamoto Y., Horiutchi T., Androck D., Androck D., Marintofi T., Manance Of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
DCP_ECOLI STANDARD; PRT; 680 AA.
P24171; P78305;
01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last annotation update)
PEPTIDYL-DIPEPTIDASE DCP (EC 3.4.15.5) (DIPEPTIDYL CARBOXYPEPTIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECURIOR 2. 7. MG1655; MEDLINE=97426617; PubMed=9278503; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION: IT IS STIMULATED BY MANGANESE, MAGNESIUM, COBALT AND CALCIUM IONS AND IS INHIBITED BY ZINC, COPPER AND
                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henrich B., Becker S., Schroeder U., Plapp R.; "dcp gene of Escherichia coll: cloning, sequencing, transcript mapping, and characterization of the gene product."; J. Bacteriol. 175:7290-7300(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997),
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MEDLINE=97251357; PubMed=9097039;
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MEDLINE=94042903; PubMed=8226676;
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Escherichia coli
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NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLL 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 KRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNL---NEDDTFLVFSKAELGALPDDFI-- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---DSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKE----ENTIILO 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLK 341
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                                                                                             34;
                                                                                                                                                                                                 ZINC (CATALYTIC) (BY SIMILARITY).
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ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                           Score 519; DB 1; Length 680;
Pred. No. 8.6e-25;
0; Mismatches 299; Indels
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04B9DCC03E15893A CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
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              MEROPS, M03.005, -. EcoGene, EG10212, dcp. InterPro, IPR001567, Peptidase_M3. InterPro, IPR00130; Zn_MTpeptdse.
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25.78;
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A49931; A49931.
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P27236;
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DCP_SALTY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1-12.
MEDLINE=92165738; PubMed=1537804;
MEDLINE=92165738; PubMed=1537804;
Miller C.G., Hamilton S.;
"Cloning and nucleotide sequence of the Salmonella typhimurium dcp gene encoding dipeptidyl carboxypeptidase.";
J. Bacteriol. 174:1656-1630(1992).
-!- FUNCTION: REMOVES TROW THE C-TERMINI OF N-BLOCKED TRIPEPTIDES, TETRAREPTIDES AND LARGER PEPTIDES.
-!- CATALYTIC REMOVES OF UNBLOCKED, C-TERMINAL DIPEPTIDES FROM OLIGOREPTIDES, WITH BROAD SPECIFICITY. DOES NOT HYDROLYSE BONDS IN WHICH PI' IS PRO, OR BOTH PI AND PI' ARE GLY.
-!- COPROCTOR: BINDS ONE ZINC ION.
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TEELIVQTKQVYDAVGMLGIEEVTYENCLQ---ALADVEVKYIVE------RTMLDFP 109
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PIR; A4229; A4229;
PIR; A4229; A4229;
REROPS; M03.005; -.
RESPONDED: PIREOUDIS: dcp.
DR InterPro; IPROUDIS: Zin_TMpeptdse.
DR PRONINS: ZinC_PROTRASE; 1.
DR PGAM; PF01432; Peptidase_M3; 1.
DR PGAM; PF01432; Peptidase_M3; 1.
DR PGAM; PF01432; Peptidase_M3; 1.
DR PGAM; PF01432; PS00142; ZinC_PROTRASE; 1.
WHOTOLISSE; Carboxypeptidase; Metalloprotease; Zinc; Dipeptidase.
METAL 469 469 BY SIMILARITY.
470 470 BY SIMILARITY.
476 ZINC (CATALYTIC) (BY SIMILARITY).
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20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDXL-DIPEPTIDASE DCP (EC 3.4.15.5) (DIPEPTIDXL CARBOXYPEPTIDASE)
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Salmonella.
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                                                                                                                                                                                                           Salmonella typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: RELEASE OF AN N-TERMINAL OCTAPEPTIDE AS SECOND STAGE OF PROCESSING OF SOME PROTEINS IMPORTED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: ACTIVITY IS DIVALENT CATION-DEPENDENT. IT IS STRUKLARDED BY MANGANESE, MAGNESIUM OR CALCIUM IONS AND REVERSIBLY INHIBITED BY ZINC, COBALT, AND IRON.
SÜBGUNIT: MONOMER.
SUBCELLULAR LOCATION: MITOCHONDENIAL MATRIX.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59) (MIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalousek F., Isaya G., Rosenberg L.E.;
"Rat liver mitochondrial intermediate peptidase (MIP): purification and initial characterization.";
EMBO J. 11:2803-2809(1992).
-I- FUNCTION: CLEAVES PROTEINS, IMPORTED INTO THE MITOCHONDRION, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 SDGVGMALFYGDFFARDSKSG-----GAMMGNFVEQSTLNFTRPVIYNVCNYQKPVDGQP
                                                                                                                                                                                                                                                                                                                                                                                                            TEELKYSIDQEFLKEYFPIE-VVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDK
                                                                                                                         343 VRREKYALDEAQLKPYFALNTVLQEGVFWTANQLFGITFVERFDIPVYHPDVRVWEIFD-
                                                                                                                                                                          ATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDG--SRMMAVAALVVNFSQPVAGRP
                                                                                                                                                                                                                                                                              SLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRR
                                                                                                                                                                                                                                                                                                     545 LSKHYKDGSPIADDLLEKLVASRLVNTG------LLTLRQIVL--SKVDQSLHTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 SLDAASEYAKYCSEILGVAATPGTNMPATFGHL-AGGYDGQYYGYLWSEVFSMDMFYSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isaya G., Kalousek F., Rosenberg L.E.; "Sequence analysis of rat mitochondrial intermediate peptidase: similarity to zinc metallopeptidases and to a putative yeast homologue."
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Mammalia; Eutheria; Rodentia;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 PTGPPGTIAQTPETVMQFLEKLSEKLCERTRKDFEMMQGMKTKLNPQ-----NSELMPWD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSF--EQMTDAHVWNKSV 418
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
4FC2E6743EA43558 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Metalloprotease; Zinc; Transit peptide; Mitochondrion; Magnesium; Manganese; Calcium; Cobalt; Iron.
TRANSIT 33 MITOCHONDRION.
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                                                                                                                                                                                                                                       MEROPS; M03.006; -.
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
Pfan; PF01432; Peptidase_M3; I.
PROSITE; PS00142; ZINC_PROTEASE; I.
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710 MI
492 ZI
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TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P.; Submitted (MAR-1994) to the EMBL/Genbank/DDBJ databases.

-!- FUNCTION: CLEAVES PROTEINS. IMPORTED INTO THE MITOCHONDRION, TO THEIR MATURE SIZE. CLEAVES THE NUCLEAR-ENCOBED PRECURSORS FOR CYTOCHROME OXIDASE SUBUNIT IV (COXIV) AND THE IRON-SULFUR PROTEIN (FE-S) OF THE BCI COMPLEX.

-!- CATALYTIC ACTIVITY: RELEASE OF AN N-TERMINAL OCTAPEPTIDE AS SECOND STAGE OF PROCESSING OF SOME PROTEINS IMPORTED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
              646
                                                                                                                                                                                                                                                                                                                                          MEDLINE-94309680; PubMed-8035833;
Isaya G., Miklos D., Rollins R.A.;
"MIPI, a new yeast gene homologous to the rat mitochondrial
intermediate peptidase gene, is required for oxidative metabolism in
                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59) (MIP).
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Interity,
Pfan, PF0143; Peptidase_M3; I.
PROSITE; P80142; ZINC_PROTBASE; I.
PROSITE; P800142; ZINC_PROTBASE; I.
PROSITE; P800142; ZINC_PROTBASE; I.
Hydrolase; Metalloprotease; Zinc; Transit peptide; Mitochondrion.
TRANSITE 38 772 MITOCHONDRIAL INTERMEDIATE PEPTIDASE.
METAL 558 558 ZINC (CATALYIC) (BY SIMILARITY).
ACT_SITE 559 559 BY SIMILARITY.
METAL 562 562 ZINC (CATALYIC) (BY SIMILARITY).
ZINC (CATALYIC) (BY SIMILARITY).
ZINC (CATALYIC) (BY SIMILARITY).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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1C19A0655FAAE7CA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.";
Mol. Cell. Biol. 14:5603-5616(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD; S0001617; OCT1.
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; zn_MTpeptdse.
                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-OCT-1996 (Rel. 34, Last seq
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88182 1
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                      OCT1 OR MIP1 OR YKL134C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             772 AA;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
Rad M.R., Xu G., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; M03.006;
                                                                                                                                                                                                                                                                                                  NCBI_TaxID-4932;
                                                                                                                                               PMIP_YEAST 8
P35999; P51980;
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29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 NNTIEKTANELKFIAELKAKDLKKPLTTNTDEILKLVRPWDRDYYTGKYFQLNPSNSPNA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFLKEYFPIEVVTEGLLNTYQELLGLSFE-QMTD-AHVWNKSVTLYTVKDKATGEVLGQF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: || : | :| :| :| :| 419 KEISYYFTLGNVIQGLSDLFQQIYGIRLEPAITDEGETWSPDVRLAVISEEEG-IIGII 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478
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                                                                                                                 SPEQIKTRTEELIVQTKQVYDAVGMLGIE--EVTYENCLQALADVEVKYIVERTMLDFPQ 110
                                                                                                                                                 85 SPDGLRKFSQVSLQQAQELLDKMRNDFSESGKLTYIMNLDRLSDTLCR-----VIDLCE 138
                                                                                                                                                                                                                               HVSS----DKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKI----KPEAR 163
                                                                                                                                                                                                                                                                                       139 FIRSTHPDDAFVRAAQ---DCHEQMFEFMNVLNTDV-----SLCNILKSVLNNPEVS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCDLFERNGKTSNPAHFTVCCSRQIYPSETDFSTIOVG-ENPDGTYFQLPVISLVCNFSP 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 -PVAGRPSL--LRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENW 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591
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                                                                                                                                                                                                                                                                                                                                                                                | ::|:| | : |: | | SKLSABELKVGKILLDDFEKSGIYMNPDVREKFIQLSQEISLVGQEF---INHTD----Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKLKPLGEAEREFILNLKKKECK----DRGFEYDGKINAWDLYYYMTQTEEL--KYSIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLDLYPREGKYNHAACF ------GLQPGCLLPDGSR - MMAVAALVVNFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TSLDAASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYS
                                                                                                                                                                                                                                                                                                                                                164 RYLE-KSIKMGK-----RNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKAELGALPDDFIDS-----LEKTDDD----KYKI-TLKYPHYFPVMKKCCIPETRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTN----
Length 772;
                                                           Indels
  12.6%; Score 461; DB 1; 25.6%; Pred. No. 3.9e-21;
                                                        Matches 176; Conservative 127; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650 CFKKEGIMNPEVGMKYRNLILKPGGSLD 677
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                                   Local
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us-09-833-782-2.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 14, 2002, 18:44:31 Run on:

; Search time 64.93 Seconds
(without alignments)
825.918 Million cell updates/sec

US-09-833-782-2 Title: Perfect score: Sequence:

1 MIARCLLAVRSLRRVGGSRI......FLKREPNQKAFLMSRGLHAP 704

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

pirl:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

microsomal endopep
thimet oligopeptid
thimet oligopeptid
saccharolysin (EC
oligopeptidase A V
oligopeptidase A (
oligopeptidase A (
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peptidyl-dipeptida dipeptidyl carboxy peptidyl-dipeptida peptidyl-dipeptida peptidyl dipeptida mitochondrial inte mitochondrial inte soluble angiotensi probable mitochond metalloproteinase metalloproteinase metalloproteinase Description SUMMARIES A43411 A45985 S43250 HYHUTH HYRTTH C82353 S47718 C82353 C47018 C64055 E83636 B81224 G81996 S76766 F75370 F82844 E82620 D85720 E64908 A42297 Query Match Length 3483 3475 2330 2330 2330 108579 848 818.5 818.5 817.5 814.5 704.5 694 690.5 631.5 635.5 627.5 578.5 520 5120 5120 495.5 448.5 415 268.5 267.5 267 Result

hypothetical prote	probable peptidase	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	rhoptry protein -	hypothetical prote	conserved hypothet	oligopeptidase - H	polyprotein allerg	oligoendopeptidase	hypothetical prote	probable coiled-co	DNA-directed RNA p	microtubule-vesicl
T27909	F82132	T00637	C83696	G70163	D72230	T28677	G71329 ·	F75103	B71934	T31423	H70130	Н72311	T41342	A64430	A43336
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820	615	1922	532	2166	852	2269	1084	880	578	1095	290	547	1115	1345	1392
5.2	4.8	4.0	3.9	3.8	3.8	3.8	3.8	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6
189	175.5	145.5	143	140	139.5	139.5	139	137.5	135	135	133.5	133	133	133	133
0	31	32	33	34	35	96	37	88	39	9	11	2	13	7	5

ALIGNMENTS

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300 360 360 420		241 301 301 361	90 AA	
240	PEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK ;	181	QY	
180	ASTEADKRLSRFDIEMSMRGDIFERIVHLOETCDLGKIKPEARRYLEKSIKMGKRNGLHL	121	Qy Db	
120 120	TEELIVOTKOVYDAVGMLGIEEVTYENCLOALADVEVKYIVERTMLDFPQHVSSDKEVRA 1 	61	Qy	
09	MIARCLLAVRSLRRVGGSRILLRWTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR 	п п	Qy	
sd	Query Match 95.0%; Score 3483; DB 2; Length 704; Best Local Similarity 94.5%; Pred. No. 1.58-203; Matches 665; Conservative 15; Mismatches 24; Indels 0; Gaps	Query Match Best Local Matches 66	ŌÆĬ	
2000 in.	soluble angiotensin-binding protein - pig C;Species: Sus Scrofa domestica (domestic pig) C;Species: Sus Scrofa domestica (domestic pig) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000 C;Accession: A4341 J; Biol: Chem. 267, 18067-18012, 1992 A;Title: Molecular cloning of porcine soluble angiotensin-binding protein. A;Meference number: A43411; MUID:92388174 A;Molecule type: mRNA A;Moscule type: mRNA Cross-references (SB:D11336; NID:9217708; PIDN:BAA01949.1; PID:9217709 A;Note: sequence extracted from NCBI backbone (NCBIN:112884, NCBIP:112886) C;Superfamily: thimet oligopeptidase C;Keywords: mitochondrion	uble a pecies ate: 3 ccessi ugiura ugiura ugiura ugiura ugiura itle: ccessi ccessi ccessi ccessi ccessi ccessi ccessi ccessi cress- ccessi		
200	pig) -Dec-1993 #text_change	ULT 411 uble a pecies	RESULT A43411 SOLUBI C;Spec C;Date	

421 YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV 480

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thimet oligo
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S43250
Bir. J. Biochem. 221, 159-165, 1994
A;Title: Cloning, amino acid sequence and tissue distribution of porcine this A;Reference number: S43250; MUID:94222057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448
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                                                                                                                                                                     29 EVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 LQETCDLGKIKPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDTFLVFSKAELGALPDDFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGEAEREFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNH
SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
                                                                                                             AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:BAA04882.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                             661 VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 2330; DB 2; 64.0%; Pred. No. 1.1e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 64.0%; Pred. No. 1.1e
Matches 431; Conservative 104; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Gross references: EMBL:D21871; NID:9456612; E.Superfamily: thimet oligopeptidase C; Keywords: hydrolase; metalloproteinase; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-687 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEQVQNEIKSMKKRMSELCIDFNKNLNEDDIFLVFSKAELGALPDDFIDSLEKTDDDKYK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 YIVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV 480
                                                                                                     900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIN:133580, NCBIP:133581)
C; Superfamily: thimet oligopeptidase
                                                                                                                                                           AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE 660
                                                                                                                                                                         1 MJARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-704 <KAW>
A;Cross-references: GB:D13310; NID:g391848; PIDN:BAA02570.1; PID:g391849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%; Score 3475; DB 2; Length 704; 93.3%; Pred. No. 4.5e-203; tive 30; Mismatches 17; Indels
                                                                                                                                                                                                                                VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 93.3% Matches 657; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA; protein
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                                                                                                                                                                                                                  199
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Thinet oligopeptidase (EC 3.4.24.15) - rat
NyAlternate names: endo-oligopeptidase A; endopeptidase 24.15; Pz-peptidase; soluble
C; Specias: Rattus norvegicus (Norway rat)
C; Date: 30-Sep-1992 #sequence_revision 17-Nov-1995 #text_change 07-May-1999
C; Accession: S38760; A54152; S55999; A36165
R; McKie, N.; Dando, P. M.; Rawlings, N.D.; Barrett, A.J.
Biochem. J. 295, 57-60, 1993
A; Reference number: S38760; MUID:94029935
A; Reference number: S38760; MUID:94029935
A; Residues: 1-687 < MCK>
R; Pierotti, A.; Dong, K.W.; Glucksman, M.J.; Orlowski, M.; Roberts, J.L.
Biochemistry 33, 622, 1994
A; Reference number: A34152; MUID:94114549
A; Contents: corrections
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                    F;451/Binding site: carbohydrate (Asn) (covalent) #status predicted F;473,477,480/Binding site: zinc (His) #status predicted F;474/Active site: Glu #status predicted
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    <MAT>
                                                                                                                                                                          Indels
  predicted
                                                                                                                             63.5%; Score 2330; DB 1;
64.9%; Pred. No. 1.1e-133;
ive 97; Mismatches 133;
  F;2-689/Product: thimet oligopeptidase #status
                                                                                                                           Query Match 63.59
Best Local Similarity 64.99
Matches 426; Conservative
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thimet oligopeptidase (EC 3.4.24.15) - human
hyputh
thimet oligopeptidase (EC 3.4.24.15) - human
NyAlternate names: beta-anyloid precursor protein processing metalloproteinase; metalloe
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Togo 1995 #sequence_revision 17-Nov-1995 #text_change 18-Jun-1999
C;Accession. 37-4197; PC4053;
R;Thompson, A.; Huber, G.; Malherbe, P.
Biochem. Biophys. Res. Commun. 213, 66-73, 1995
A;Title: Cloning and functional expression of a metalloendopeptidase from human brain wi
A;Accession: JC4197; MUID:95387027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si C; Superfamily: thimet oligopeptidase C; Keywords: Alzheimer's disease; amyloid; brain; glycoprotein; hydrolase; metalloprotein
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A; Residues: 67-78;181-197, /x',199-200 <PAP>
A; Experimental source: brain of Alzheimer's disease patient
A; Note: sequence modified after extraction from NCBI backbone
C; Comment: This metalloproteinase is responsible for cleaving a Met-Asp bond in the A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Identification of a metalloprotease from Alzheimer's disease brain able A;Reference number: A53633; MUID:94114484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U29367: NID:g1098597; PIDN:AAA82606.1; PID:g1098598 R;Papastoitsis, G.; Siman, R.; Scott, R.; Abraham, C.R. Biochemistry 33, 192-199, 1994 A;Title: Identification of a metalloprotease from Alzheimer's disease brain a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN: AAA82607.1; PID: 91098600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-689 <THO1>
A;Cross-references: GB:Z50115; NID:g1030054; PIDN:CAA90477.1; PID:g1030055
425 AACFGLQPGCLRQDGSRQIAIAAMVANFTKPTPDAPSLLQHDEVETYFHEFGHVMHQLCS 484
                                                                QTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRL
                                                                                                                                                                                                                  YDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKR
                                                                                                                             VNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEILGVAATPGTNMPATFGHLAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:THOP1; GDB:ME78
A;Cross-references: GDB:595011; GDB:642232; OMIM:601117
A;Map position: 19q13.3-19q13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross references: EMBL:U29366; NID:g1098599; R; Munroe, D.G. submitted to the EMBL Data Library, June 1995 A; Accession: G01882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: brain
A; Accession: PC4053
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
B; Munroe, D.G.
B; Munroe, D.G.
B; Munroe, D.G.
B; Mitted to the EMBL Data Library, June 1995
A; Reference number: H00694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-5 <MUN2>
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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DPKQDAFLLSKGL 677
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A;Cross-references: GB:X76504; NID:q531547; PIDN:CAA54039.1; PID:q531548
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 541-R;Defoor, B.; Debrabandere, R.; Keyers, B.; Voet, M.; Volckaert, G.
A;Tette: Nucleotide sequence of D10B, a BamHI fragment on the small-ring chromosome I A;Reference number: S25338; MUID:93070606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yscD). Structure, function and relationship
                                                                                                                                                                                                                                                                                                                                saccharolysin (EC 3.4.24.37) - yeast (Saccharomyces cerevisiae)
N,Alternate names: protein YCL057w; protein YCL434; proteinase yscD
C;Species: Saccharomyces cerevisian 31-Mar-1992 #text_change 26-Aug-1999
C;Accession: S19387; S19745; S41110; S25341
R;Alexandrath, D.; Galland, P.; Thireos, G.; Tzermia, M.
asubmitted to the Protein Sequence Database, March 1992
A;Reference number: S19387
645
                                                         621
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586 QSLHTNTSLDAASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMD
                               4 LLCKNWFASPVISPLLYTRSLYSMANTTSFPIAPQAPPNWSFTPSDISGKTNEIINNSNN
                                                                                                                     646 MFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL 701
                                                                                                                                                     37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: S41110
A, Status: not compared with conceptual translation
A, Molecule type: DNA
A, Residues: 1-712 <BUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: not compared with conceptual translation A;Molecule type: DNA
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C;Keywords: hydrolase; metalloproteinase; zinc
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A;Cross-references: SGD:S0000562; MIPS:YCL057w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Accession: S19745
A.Molecule type: DNA
A.Residues: 663-712 <VVOES
A.Cross-references: EMBL:X59720; MIPS:YCL057w
R.Buechler, M.; Tisljar, U.; Wolf, D.H.
EUI. J. Biochem, 219, 627-639, 1994
A.Title: Proteinase yscD (oligopetidase yscD)
A.Reference number: S41110; MUID:94139744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X59720; MIPS: YCL057w
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A; Residues: 1-663 <ALE>
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                      A.Molecule type: mRNA

A.Residues: 320-350-578-597,'F',599-687 <PIE>
A.Residues: 320-350-578-597,'F',599-687 <PIE>
A.Residues: 320-350-578-597,'F',599-687 <PIE>
A.Note: Hole report is a correction to A36165

A.Note: His report is a correction to A36165

R.McKie, N.; Dando, P.M.; Brown, M.A.; Barrett, A.J.

Biochem. J. 309, 203-207, 1995

A.Title: Rat thimet oligopeptidase: large-scale expression in Escherichia coli and chara A;Reference number: S55999; MUID:95344370

A.Accession: S55999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Cross-references: GB:M61142
A; Note: parts of this sequence, including the amino end of the mature protein, were conf
C; Comment: This enzyme is found in testes, brain, and pituitary predominantly in a soluk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: hydrolyzes peptide bonds on the carboxyl side of hydrophobic residues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Molecular cloning and primary structure of rat testes metalloendopeptidase A,Reference number: A36165; MUID:91084500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVLRWDLSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKEC 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 EQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSR 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 NHLRWDLSAQQIRALTTQLIEQTKCVYDRVGAQDFEDVSYESTLKALADVEVTYTVQRNI 81
                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1.9 <MC2>
A; Note: this 1s an engineered sequence expressed in Escherichia coli
R; Plerotti, A.; Dong, K. W.; Glucksman, M.J.; Orlowski, M.; Roberts, J.L.
Biochemistry 29, 10323-10329, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: thimet oligopeptidase
C; Keywords: hydrolase; metalloproteinase; oligopeptidase; zinc
F; 2-687/Product: thimet oligopeptidase #status predicted <WAT>
F; 473, 477, 480/Bining site: zinc (His) #status predicted
F; 474/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: significant sequence differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A36165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Function:
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Qy 241 ITLKYPHY : Db 240 VTFKYPDI	ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA 300 	OY 227 FIDSLEKTDDDKYKITLKYPHYFPVMKKCIPFTRRRMEMAFNTRCKE 274 : : : :
Qy 301 DFVLEMNT :: Db 299 NYNLYDKN	DEVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD 360 ::	QY 275 ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAER 334 : : : : : : : : : : Db 254 DNSEIIAEQLKLRHEIARMLGFSTYSEKSLATKMAQTTDQVLGFLNDLANKAKPQGEREV 313
Qy 361 LYYYMTQT : Db 359 HRYYDNKY	LXXXMTQTEELKXSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWN 415 : :: : : : :	OY 335 EFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTBGLL 394 :
Qy 416 -KSVTLYT ::: Db 419 VKQIAVWN	416 -KSYTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVV 474 : :: : : :	QY 395 NTYOELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGL 454
Oy 475 NFSQPVAC : Db 479 NFSKSTKI	NFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQIDFARFSGT-NVETDFVEVPSQMLE 533 : : : :	QY 455 QPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDBVRTYFHBFGHVMHQICAQTDFAR 514 1
Oy 534 NWVWDVDS : Db 539 FWTWNKNE	NWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTS 593 -	QY 515 FSGTN-VETDFVEVPSQMLENWWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGL 573
QY 594 LDAASE : Db 599 LQNLSICI	LDAASEYAKYCSEILGVAATPGTNMPATFGH-LAGGYDGQYYGYLWSEVFSMDMFY 648	QY 574 LTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI-LGVAATPGTNMPATFGHL-AGG 628
Oy 649 SCFKKEG1 : : Db 659 TKFAKDP-	SCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL 701 :	QY 629 YDGQYYGYLWSEVFSWDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKR 688
RESULT 7 C82353 C1190eptidase A VC0188 C)Species: Vibrio chole C;Date: 18-Aug-2000 #se C;Accession: C82353 R.Heidelberg, J.F.; Eis Rhurdson, D.; Ermolaeva J. R.R.; Mekalanos, J.J Nature 406, AT7-483, 20 A.Title: DNA Sequence o A.Reference number: A82 A.Accession: C82353 A.Status: preliminary A.Molecule type: DNA A.Rosidues: 1-680 AHEI-A A.Cross references: GB: A.Gene: VC0188 A.Hap position: 1 C;Genetics: A.Gene: VC0188 A.Map position: 1 C;Genetics: A.Gene: VC018 A.Map position: 1 C;Superfamily: peptidyl Cuery Match Best Local Similarity Matches 209; Conser Oy 52 LSPEQIKTRTEEL Db 17 IKPEHVKPAVEQA OY 112 VSSDKEVRAASTE	VC0188 [imported] - Vibrio cholerae (strain N16961 serogroup 01) cholerae 00 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 3: Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Olaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. 33, J.000 ence of both chromosomes of the cholera pathogen Vibrio cholerae. 1: A82035; MUID:20406833 nary DNA CHES> s: GB.EE004109; GB.EE003852; NID:99654590; PIDN:AAF93364.1; GSPDB:GN001 urce: serogroup 01; strain N16961; biotype El Tor 23.1%; Score 848; DB 2; Length 680; ptidyl-dipeptidase Dcp ptidyl-dipeptidase Dcp ptidyl-dipeptidase Dcp ptidyl-dipeptidase Dcp ptidyl-dipeptidase Dcp pridyl-dipeptidase Dc	Oy 689 EPROKAFMASGIAN 703 Db 666 EPQIDALLRHAGIAN 680 RESULT 8 S47718 Oligopeptidase A (EC 3.4.24) - Escherichia coli 0.14gopeptidase A (EC 3.4.24) - Escherichia coli pric encodes an endopeptidase and is homologous to the Salm 0.14gopeptidase A (EC 3.4.24) - Escherichia coli 0.14gopeptidase A (EC 3.4.24) - Escherichia coli pric encodes an endopeptidase and is homologous to the Salm 0.14gopeptidase A (EC 3.4.24) - Escherichia coli 0.14gopeptidase A (EC 3.4.24) - Escherichia coli 0.14gopeptidase A (EC 3.4.24) - Escherichia coli 0.14gopeptidase A (EC 3.4.4.4) - Escherichia coli 0.14gopeptidase A
QY 172 MGKRNGLE	172 MGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDD 226	A;Status: preliminary A;Molecule type: DNA

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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Teference number: Ad4000; MUID:95350630
A;Accession: C64055
A;Accession: C64055
A;Accession: C64055
A;Molecule type: DNA
A;Residues: 1-681 </TICR>
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C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C;Accession: C64055
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C,Superfamily: peptidyl-dipeptidase Dcp
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A;Residues: 1<sup>4</sup>42,'E',44-210,'FV',213-264,'AA',267-389,'H',391-405,'T',407-515,'G',517-6θ
A;Note: sequence extracted from NCBI backbone (NCBIN:113030, NCBIP:113031)
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A;Titles Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: B86021
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                                                                                                                                                                                                                                                             Length 680;
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                                                                                                                                                                                                                                                       22.3%; Score 818.5; DB 2; ilarity 31.9%; Pred. No. 4.6e-42; Conservative 122; Mismatches 276;
                                                                                             A,Gene: prlC
C,Superfamily: peptidyl-dipeptidase Dcp
C,Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                                                                                       Local Similarity
nes 206; Conserv
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A, Gene: prlC
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GB:L42023; NID:g1573170; PIDN:AAC21882.1; PID:g1573174

C; Keywords: hydrolase; metalloproteinase

C; Keywords: hydrolase; metalloproteinase

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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: E838536
A;Status: preliminary
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83636
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ... Lory, S.; Olson, M.V.
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A; Residues: 1-681 <STO>
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Best Local S
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J. Bacteriol. 174, 1631-1640, 1992
A;Title: Cloning and nucleotide sequence of opdA, the gene encoding oligopeptidase A
A;Reference number: A42298; MUID:92165739
A;Accession: A42298
                                 15;
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N;Alternate names: endo-oligopeptidase A
C;Species: Salmonella typhimurium
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 29-Sep-1999
C;Accession: A42298
                                                                                                                                               IDSLEKTDDDK----YKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKE-----E 275
                                                                                                                                                                                                                                                                        NTIILQQLEPERTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAERE 335
                                                                                                                                                                                                                                                                                                                                          FILNLKKKECKDRGFEYDG--KINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGL 393
                                                                                                                                                                                                                                                                                                                                                                                                       ELKGYCEKEF-----GVTELAPWDIGFYSEKQKQHLYAINDEELRPYFPENRVISGL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 LNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHA---A 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFARFSGIN-VETDEVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLV 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                570 NTGLLTLRQIVLSKVDQSLH-----TNTSLDAASEYAKYCSEILGVAATPGTNMPATF 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIK 171
                                                                                                                                                                                         172 MGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTF----LVFSKAELGALPDDF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHL-AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDM 681
                                                             52 LSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQH 111
                                   Gaps
                                                                                           IKPEHIRPAVEKLIQDCRNTIEQV -- LKQPHFTWENFILPLTETNDRLNRAWSPVSHLNS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;MOLECULE type: DNA
A;Residues: 1-680 <CON>
A;Cross-references: GB:M84574; NID:g154213; PIDN:AAA27172.1; PID:g154214
C;Superfamily: peptidyl-dipeptidase Dcp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544 QAAMFILRQLEFGIFDFRLHHTFDAEKTNQILDTLKSVKSQVAVIKGV---DWARAPHSF
                                 49;
   Length
                                 Indels
Query Match 22.2%; Score 814.5; DB 2; Best Local Similarity 30.3%; Pred. No. 8e-42; Matches 206; Conservative 127; Mismatches 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHNFLKREPNQKAFLMSRGL 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALAAAKAQAEAKEQECYLLTLDIPSYLPVWTYCDNOALREEWYRAYSTRASDQCPNAGK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SISTATEMENTALE SINGLE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNSVKNSPELREAYEQTLPLLSEYSTWVGQHEGLYNAYRDLRDGDHYATLNTAQKKAVDN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDD---TFLVFSKAELGALPD 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFIDS----LEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNIRC-----K 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFILNLKKKECKDRGFEYDGKINAWDLYYMTQTEELKYSIDQEFLKEYFPIEVVTEGL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511 DFARFSG-TNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLV 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAALFILRQLEFGLFDFRLHAEFNPQQGAKILETLFEIKKQVAVVPSPTWGRFPHAFSHI 602
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                                                                                                                                                                           Gaps
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                                                                                                                                                                  42;
                                                                                                                                                                  Conservative 129; Mismatches 300; Indels
        Length
22.0%; Score 806; DB 2; 30.4%; Pred. No. 2.6e-41;
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M.J.,

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GB:AE002098; NID:97225435; PIDN:AAF40670.1; PID:9722
B, strain MC58
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                                                                           A)Cross-references: GB.AE002379; GB.A.Experimental source: serogroup B, C,Genetics: MA:Gene: NAMB0214
C;Superfamily: peptidyl-dipeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673
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                                                     1-678 <TET>
A; Status: preliminary
                            A; Molecule type: DNA
                                                           A; Residues:
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R) Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; VA; Reference genome sequence of Neisseria meningitidis serogroup B strain MC58.

A; Accession; B81224
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                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517 GTN-VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLT 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 TIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREF 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 YOELLGLSFEOMTDAHVWNKSVTLYTVKDKATGEVLGOFYLDLYPREGKYNHAACFGLQP 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607
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                                                                                                                                                                                                                                                                                                   LSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQH 111
                                                                                                                                                                                                                                                                                                                                                                                                                       112 VSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFRLSGIDLPADKOKRYAEVOSRLSELGSRFSNQLLDATQAWTKHVTDEAALAGLTDSAK 197
                                                                                                                                                                                                                                                                                                                                                               18 IRPEHVKPAIERILADNRAAIARLLETQREQPTWKGLVLAMDELNDRLGAAWSPVSHLNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 GPVMEEILDIRQELAGLIGFANYAELSLATKMAESSDQVLSFLRDLAVRSKPFAARDLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 ILNLKKKECKDRGFEYDGKINAMDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L----RAYAAEQGCT----ELQSWDAGYYAEKLREARYSVSQEALRAYFPVDKVLSGLFAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 GCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFS
                                                                                                                                                                                                                                           31;
                                                                                                                                                                                  Length 681;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                         Query Match 21.7%; Score /94.5; Ub 4, Best Local Similarity 30.1%; Pred. No. 1.3e-40; Matches 202; Conservative 132; Mismatches 305;
                                                        A;Gene: prlC; PA0067
C;Superfamily: peptidyl-dipeptidase
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Experimental
                               C;Genetics:
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RESULT 14
681996
6.190peptidase A (EC 3.4.24.70) NMA0054 [imported] - Neisseria meningitidis (strain Z cligopeptidase A (EC 3.4.24.70) NMA0054 [imported] - Neisseria meningitidis
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C; Accession: G81996
R; Parkhill, J; Achtman, M; James, K.D; Bentley, S.D; Churcher, C.; Klee, S.R; Mo; Holroyd, S.; Jagels, K; Leather, S.; Moule, S.; Mungall, K; Quall, M.A.; Rajandre Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
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                                                   Gaps
                                                                                                      55 EQIKTRTEELIVQT--KQVYDAVGMLGIEEVT-YENCLQALADVEVKYIVERT----ML 106
                                                                                                                                                      70
                                                                                                                                                                                                                                            107 DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL
                                                                                                                                                                                                                                                                                                               EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL
                                                                                                                                                                                                                                                                                                                                             224 PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 DLAEVKAFARE-SLNL------ADLQPWDLGYASEKLREAKYAFSETEVKKYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 VASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534 LAAKNFQRGMFLVRQMEFALFDMMIYSEDDEGRLKNWQQVLDSVRKKVAVIQPPEYNRFA
                                                                                                                                                      16 DQIKTEDIKPALQTAIAEAREQIAAIKAQTHTGWANTVEPLTG----ITERVGRIWGVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 -TFGHL-AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDG
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Query Match 19.1%; Score 702; DB 2; Length 676 Best Local Similarity 28.4%; Pred. No. 5.2e-35; Matches 194; Conservative 126; Mismatches 302; Indels
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198
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A;Reference number: A81775; MUID:20222556
A;Accession: G81996
A;Status: preliminary
A;Accession: G81996
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-678 cPAR>
A;Residues: pric: NAA0054
C;Superfamily: peptidy1-dipeptidase Dcp
C;Reywords: hydrolase; metalloproteinase
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S7676
S7676
SPORT 15
SYNECHOCYSTIS SP. (strain PCC 6803)
C; Species: Synechocystis Sp.
A; Varitety: PCC 6803
C; Satzlety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Accession: S76766
                                                                                                                                                                                                                                                                                                                                         EQIKTRTEELIVQT--KQVYDAVGMLGIEEVT-YENCLQALADVEVKYIVERT-----ML 106
                                                                                                                                                                                                                                                                                                                      DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 GLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDF 512
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                                                                                                                                                                                                  Length 678
                                                                                                                                                                                               Query Match
18.9%; Score 694; DB 2; Lengtn b/s
Best Local Similarity 28.2%; Pred. No. 1.6e-34;
Matches 190; Conservative 131; Mismatches 309; Indels
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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to the EMBL Data Library, June
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLTALEEKLSWTWGTVSHLMGVKNSPELRHGFEQVQPLVVGFISRLGQSRPLYEAFVALR 137
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                                                                                                                                A; Reference number: S74322; MUID:97061201
A; Reference number: S76766
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-713 <KAN>
A; Cross-references: EMBL:D90916; GB:AB001339; NID:91653715; PIDN: A; Note: the nucleotide sequence was submitted to the EMBL Data L: C; Genetics:
A; Start codon: GTG
C; Superfamily: peptidyl-dipeptidase Dcp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.8%; Score 690.5; DB 2; Best Local Similarity 27.9%; Pred. No. 2.8e-34; Matches 196; Conservative 137; Mismatches 315;
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Search completed: January 14, 2002, 18:57:49 Job time: 798 sec

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(without alignments)
1371.775 Million cell updates/sec
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Sequence 11, Appl
Sequence 1153, A
Sequence 8169, Appl
Sequence 51, Appl
Sequence 64, Appl
Sequence 11338, A
Sequence 15046, A
Sequence 15045, A
Sequence 15045, A
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Sequence 1906, Ap
Sequence 19883, A
Sequence 19882, A
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Sequence 6498, Ap
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Sequence 57, Appl
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                                                                               ; Search time 18.45 Seconds
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cgn1_6/ptodata/1/paa/NGO6_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/USO0_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-897-516-6498

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US-09-806-866-55

US-09-806-866-55

US-09-806-866-51

US-09-708-427-15045

US-09-708-427-19883

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                                                                                                                                                                                                                                   170028 segs, 35950645 residues
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                                                                             January 14, 2002, 18:54:36
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Maximum Match 100%
Listing first 45 summaries
                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Sequence 449, App Sequence 12952, A	Sequence 512, App			Sequence 19312, A		-		Sequence 9203, Ap	Sequence 21161, A		Seguence 21159, A	Sequence 4897, Ap	Sequence 2855, Ap	Sequence 2854, Ap	Sequence 2853, Ap
US-60-337-358-449 US-09-708-427-12952	US-60-337-358-512	US-09-708-427-19314	US-09-708-427-19313	US-09-708-427-19312	US-09-815-242-11489	US-09-708-427-9205	US-09-708-427-9204	US-09-708-427-9203	US-09-708-427-21161	US-09-708-427-21160	US-09-708-427-21159	US-09-815-242-4897	US-09-708-427-2855	US-09-708-427-2854	US-09-708-427-2853
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111	109.5	109.5	109.5	109.5	108	107.5	107.5	107.5	107	107	107	106.5	106.5	106.5	106.5
27	53 30	31	32	33	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Spiridonov, Sergei
TITE OF INVENTION: Xenorhabdus Sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
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Best Local Similarity 30.2%; Pred. No. 9e-47;
Matches 207; Conservative 126; Mismatches 295; Indels
                                                                   Sequence 6500, Application US/09897516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Xenorhabdus sp.
US-09-897-516-6500
US-09-897-516-6500
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US99/25373
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 60/103,794
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: 60/132,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/09806866 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scarlato, Vincenzo
Rappuoli, Rino
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SOFTWARE: PatentIn version 3
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Tettelin, Herve
Venter, J. Craig
Masignani, Vega
Galeotti, Cesira
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Scarselli, Maria
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                 EFILNLKKKECKDRGFEYDG--KINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEG 392
                                     450 ACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQ 509
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APPLICANT: Balvar, Thomas M.
APPLICANT: Stater, Steven M.
APPLICANT: Spridonov, Sergei
TITLE OF INVENTION: Schoolus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)8
CURRENT APPLICATION NUMBER: US/09/897,516
FILE REFERENCE: 2001-06-29
FRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: SU00-06-30
FRIOR FILING DATE: SU00-06-30
FRIOR FILING DATE: SU00-06-30
FRIOR FILING DATE: SU00-06-30
                                                                                   393 LLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHA---
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina
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US-09-897-516-6498
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                                                                                                  344 E-CKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLG 402
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TITLE OF INVENTION: Neisseria Genomic Research
FILE REFERENCE: CHIR-0313
CURRENT APPLICATION NUMBER: US/09/806,866
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: PCT/US00/05928
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                                                                                                                                                                     EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
                                                                                                                                                                                                                                                                                       275 --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA 332
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                             20;
  Length 678
19.1%; Score 702; DB 5; Length 67 illarity 28.7%; Pred. No. 2.2e-40; Conservative 127; Mismatches 305; Indels
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Scarselli, Maria
Scarlato, Vincenzo
Rappuoli, Rino
Pizza, Mariagratia
Grandi, Guido
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Masignani, Vega
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Tettelin, Herve
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TITLE OF INVENTION: Neisseria Genomic Research
       HILLE REFERENCE: CHIR 0313; CURRENT APPLICATION NUMBER: US/09/806,866; CURRENT FILING DATE: 1999-10-08
PRIOR PRILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-10-08
PRIOR PLICATION NUMBER: PCT/US99/25373
PRIOR PLICATION NUMBER: 60/103,794
PRIOR PLICATION NUMBER: 60/103,794
PRIOR PLILING DATE: 1999-10-09
PRIOR PLILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 57
                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-806-866-57
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Best Local, Similarity 28.2%; Pred. No. 7.7e-40;
Matches 190; Conservative 131; Mismatches 309;
                                                                                                                                                                                                                                                           APPLICANT: Pizza, Mariagratia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Research
                                                                                                                                                                                                                                                                                                         TILLE REPERENCE: CHIR-0313
CURRENT APPLICATION NUMBER: US/09/806,866
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: PCT/US00/0528
PRIOR APPLICATION NUMBER: PCT/US99/25373
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1998-10-09
SAGNEMARE: PATENTIN VERSION 3.1
SEQ ID NO 55
LENGTH: 678
Application US/09806866
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US-09-806-866-55
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Rappuoli, Rino
                                                                                                            APPLICANT: | Venter, J. Craig
APPLICANT: | Masignahi, Vega
APPLICANT: | Galeotti, Cesira
APPLICANT: | Mora, Manrosa
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Scarselli, Maria
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572 GLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA-TFGHL-A 626
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Pred. No. 7.7e-40;
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TITLE OF INVENTION: Neisseria Genomic Research
FILE REFERENCE: CHIR-0313
FILE REFERENCE: CHIR-0318
CURRENT APPLICATION NUMBER: US/09/806,866
CURRENT FILING DATE: 1999-10-08
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US99/25373
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 60/103,794
PRIOR PLICATION NUMBER: 60/103,794
PRIOR PPLICATION NUMBER: 60/132,068
PRIOR PELING DATE: 1999-04-30
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Scarlato, Vincenzo
Rappuoli, Rino
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SOFTWARE: PatentIn version 3.1
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Tettelin, Herve
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Galeotti, Cesira
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Best Local Similarity
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425 513

311 394 572

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690

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--FAELSAFAARELGID---TLQPWDVPFASDRLRAARYAVDEQEVRAHFPVERVIAGWQ 366
     395 NIYQELLGLSFEQMIDAHVWNKSVILYIVKDKAIGEVLGQFYLDLYPREGKYNHAACFGL 454
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                                                                                                                                                                                                                                                                                                                                                     193 DMAIFADAAKARGLEGWVVTLQAPSVSAVLTFAENRDLRARLYRAYGTRASDQGPHAGQF
                                                                                                                        ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAER
                                                                                                                                                                                         EFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLL
                                                                                                                                                                                                                                                                                               367 ALLARLFGVRLVARPDVAVYHPDACYYDVVD-AEGVVIAGVYTDLHARAGKRSGAWMAQA
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                                                      D---FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKE
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Ge.
FILE REFERENCE: 38-21(51847)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corbin, David R.
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; ORGANISM: Xenorhabdus sp.
US-09-897-516-8169
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Best Local S:
Matches 163,
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Sequence 11537, Application US/10015127

GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof FILE REPERENCE: 38.10(15806)B

CURRENT APPLICATION NUMBER: US/10/015,127

CURRENT FILING DATE: 2001-10-29

PRIOR PLILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 14357

SEQ ID NO 11337
                                                                                                                            112 VSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEA-RRYLEKSI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 KMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAE-----LGALPD 225
                                                                                                                                                                                                                                              LINTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACF 452
                                                                                                                                                                                                                                                                     GLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEI----LGVAATPGTNMPA-TFGHL-A 626
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NHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDDAAPLAGI 190
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                                                                                                                                                                                                                                                                                                                                   542 GMFLVRQMEFALFDMMIYSEDDEGRLKNWQOVLDSVRKEVAVVRPPEYNRFANSFGHIFA
                                  PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKE----
                                                                                                        --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDUSQKLKPLGEA
                                                                                                                                                                           EREFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEG
                                                                                                                                                                                                                                                                                                                 453 GLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 IHPDQIAPALDAVIAEHQAAVERV--IASESRSFDDVWMPLERAETAIDALWSTVSHLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Sphingomonas elodea
US-10-015-127-11537
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Best Local Similarity
Matches 189; Conserv
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US-10-015-127-11537
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                                          160 DADKIKMKALNQEAATLRIQFINKLLAATKDGALTIKDKTLLAGLSDGEMAAAAQAASER 219
                                                                                                                       220 KLDNOWLFVLQNTTQQPVLQDLKDRTRKALFEASWNRAEKGDDNDTRQTLSRLAKIRAE 279
                                                                                                                                                                                                  280 QAKLLGFKDYASWKLQSQMAKTPEVALKFLRD----IVPAATARAE------REAKDIQ 328
                                                                                                                                                                                                                                                                                  LLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGK------YNHAA 450
                                                                                                                                                                                                                                                                                                                                                                           CFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQT 510
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                                                                                    TODDKYKITLKYPHYFPVMKKCCIPETRRM-EMAFNTRCK---EENTIILQQLLPLRTK 289
                                                                                                                                                                        290 VAKLIGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKD-- 347
                                                                                                                                                                                                                                                        -----RGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPI-EVVTEGLLNTYQE 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGHL-AGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMD
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APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Research
FILE REFERENCE: CHIR-0313
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CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: PCT/US00/05928
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 60/103,794
PRIOR APPLICATION NUMBER: 60/103,794
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1999-10-03
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Masignani, Vega
Galeotti, Cesira
Mora, Manrosa
Ratti, Giulio
Scarselli, Maria
Scarstalti, Maria
Rappuoli, Rino
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347 DRGFEYD-----GKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQE 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 KLLGYSTHADFVLEMNTAKST----SRVTAFLDDLSQKLKPLGEAEREFILNLKKKECK
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                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: (289)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (313)..(313)
OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
LOCATION: 7300.
                                                                                                                                                       any amino acid
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                                                                        ORGANISM: Neisseria meningitidis
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PatentIn version 3.1
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OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
                                                                                                                                   LOCATION: (149)..(149)
OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa
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                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (158)..(158)
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LOCATION: (331)..(331)
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LOCATION: (445)..(445)
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Best Local Similarity
Matches 139; Conserv
                SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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Sequence 44, Application US/09826734
GENERAL INFORMATION:
APPLICANT: Fernandes, Elma R.
APPLICANT: Vernet, Corine A.M.
APPLICANT: Mishra, Vishnu S.
APPLICANT: Ashlar, Vishnu D.
APPLICANT: Ashlar, Richard A.
APPLICANT: Ashlar, Bryan D.
APPLICANT: Kekuda, Ramesha
TILLE OF INVENTION: NOVel Polynucleotides and Polypeptides Encoded Thereby
FILE REFERENCE: 15966-754
CURRENT APPLICATION NUMBER: US/09/826,734
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
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GENERAL INFORMATION:
APPLICANT: BOWEr, Stanley G.
APPLICANT: Hinkly G.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof
                                                                                                                                                                                                                                                                                                                  EREFILNLKKKECKDRGFEYDGKIN--AWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVT 390
                                                                                                                                                                                                                                                                                           EGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAA 450
                                                                                                                                                                                                                                                                                                                                                                                451 CFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQT 510
                                                         191 PEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYYTRASELSNDG
                                                                                                                                                                                                                               D-----LAEVKAFAREHLGLADPQPWDLSYAGEKLREAKYAFSETEVKKYFPVGKVL
                           PDD----FIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKE----
                                                                                                                --ENTIILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 270
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
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ORGANISM:
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                                                                       347 XEFALFDAMIYSEDDEGRLKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIFAGGYSAAX 406
227 FSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHHLLTQVDELGVSGIN 286
                                           520 -VETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQ 578
                                                                                                                                579 IVLSKVDQSLHTNTSLDAASEYAKYCSEI---LGVAATPGTNMPA-TFGHL-AGGYDGQY 633
                                                                                                                                                                                                                      634 YGYLWSEVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQK 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 DFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 SHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFATLSPAQKTKL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKN-LNEDDTFLVF--SKAELGAL 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 QIKTEDIKPAVQT-AIAEARGQIAAVKAQTHTGWANTVERLTG-----ITERVGRIWGVV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 475; DB 5; Length 491; 28.0%; Pred. No. 5.4e-25; Live 88; Mismatches 222; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pizza, Mariagratia
APPLICANT: Grandi, Guido
TITLE OF INVERTION: Nelsseria Genomic Research
FILE REFERENCE: CHIR-0313
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PRIOR APPLICATION NUMBER: PCT/USO0/05928
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-10-08
PRIOR PLICATION NUMBER: PCT/US99/25373
PRIOR PLICATION NUMBER: 60/103,794
PRIOR PLICATION NUMBER: 60/103,794
PRIOR PLILNG DATE: 1999-10-09
PRIOR PLILNG DATE: 1999-10-09
PRIOR PLILNG DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 1999-10-08
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US-09-806-866-59; Sequence 59, Application US/09806866; GENERAL INFORMATION:
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US-09-806-866-59
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Ratti, Giulio
Scarselli, Maria
Scarlato, Vincenzo
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Masignani, Vega
Galeotti, Cesira
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Peterson, Jeremy
Tettelin, Herve
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Best Local Similarity
Matches 137; Conserv
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APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT PAPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTHARE: Patentin version 3.1
SEQ ID NO 15045
LENGTH: 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ELGALPDDFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNTRCKEENTI 278
                                                                                                                                                                                 -----QTVVQE-----NEELRERETA 706
                                                                                                                                                                                                                                                   279 ILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFIL 338
                                                                                                                                                                                                                                                                                                                                                                                           NIKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQ 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       765 ELHGMVVEIEDLRSKDSLAQKKI------EELSNFNASLLIKENELQAVVCENE 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           813 ELKSKQVSTLKTIDELSDLKQSLIHKEKELQ--AAIVENEKLKAEAALSLQRIEELTNLK 870
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                                                                                                                                                                                                                                                                                                                  ----EELSKLHEILSDQETKLO-----IS 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ETAYLKKIEELSKVQEDLLNKEN 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LOPGCLLPDGSRMMAVAALVVNFSOPVAGRP 484
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             399 ELLGLSFE----QMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 SLL--RHDEVRTYFHE-------FGHVMHQICAQTDFARFSGTNVETDFVEVP
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18.2%; Pred. No. 1;
Live 84; Mismatches 194; Indels 220;
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; OTHER INFORMATION: Ceres Seq. ID 1828628
US-09-708-427-15045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 15045, Application US/09708427; GENERAL INFORMATION:
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LOCATION: 1..1304
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LOCATION: 1..1304
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ORGANISM: Arabidopsis
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US-09-708-427-15045
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TAPLICAMEN:
TITLE OF INVENTION:
TITLE OF I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 -----QHIDQEAEELRGREASHLKKIEELSKE---NENLVDNVANMQNIAEESKDL 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               535 WVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSL 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WALDPKVLPHYAVNYKDGSVIPQALVDKIKRAGTFNSGYSFGEALAAAEMDMSWHSLAAA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 NFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLEN 534
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18.2%; Pred. No. 0.86;
tive 84; Mismatches 194; Indels 220; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           649 SCFRKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 338.5; DB 6;
31.9%; Pred. No. 5e-16;
tive 45; Mismatches 108;
; FILE REFERÈNCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; NUMBER OF FEQ ID NOS: 14357
; SEQ ID NO 11338
; LENGTH: 251
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LOCATION: 1..1144
OTHER INFORMATION: Xaa is any amino acid
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US-10-015-127-11338
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Matches 75, Conservative
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VETSION 3.1
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159 KPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKA 218
                                                                                                                       279 ILQQLLPLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFIL 338
                                                                                                                                                                                   NLKKKECKDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQ 398
                                                                                                                                                                                                                                                                                                               ------LQPGCLLPDGSRMMAVAALVVNFSQPVAGRP 484
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                 ELGALPODFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTI
                                                                                        ELSELNESLVDKASKL------OTVVQE-----NEELRERETA
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COCATION: 1..1313
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1..1313
COTHER INFORMATION: Ceres Seq. ID 1828627
US-09-708-427-15044
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US-09-708-427-15044
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                                                                                                                                                                                                                                                                                                                                                                                                                                             876 YLKKI------IS
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Search completed: January 14, 2002, 19:00:16 Job time: 340 sec

C 13 376.8 17.8 680 11 BG380774 BG380774 UI-R-CTO-14 373.2 17.6 675 11 BF719641 AA152501 AA152501 AA152501 AA152501 AA152501 AA162501 CONTAGU.X CO	250.6 11.8 748 11 BG972692 BG972692 60283890 ALIGNMENTS ALIGNMENTS ALIGNMENTS TION WF50b06.x1 NCI_CGAP_Ut1 Homo sapiens CDNA clone IMAGE:2491091 3' similar to SW:NEUL_PIG Q02038 NEUROLXSIN PRECURSOR ;, mRNA sequence. TON A1952756.1 GI:5745066 N A1952756.1 GI:5745066 N A1952756.1 GI:5745066 NISM Homo sapiens EST 08-MAR-2000 NENA POTENTIAL SW:NEUL_PIG Q02038 NEUROLXSIN PRECURSOR ;, mRNA sequence. NISM Romo sapiens ENT. NISM Homo sapiens ENT. Hominidae: Homo.	nih.gov/ncicgap. ncer Genome Anatomy Proj h.D. er Moskaluk, M.D., Ph.D. fe Technologies, Inc. g Lennon, Ph.D. n University Genome Seq clone distribution inf consortium/LLNL at: nage.html or: 0.00
	3: em_estin:* 6: em_eston:* 7: em_estp:* 8: em_estp:* 7: em_estro:* 8: em_estco:* 10: gb_est:* 11: gb_est:* 12: gb_htc:* 13: gb_gss:* 14: em_gss_inv:* 15: em_gss_inv:* 16: em_gss_pin:* 17: em_gss_pin:* 18: em_gss_pin:* 21: em_gss_pin:* 22: em_gss_pir:*	th d th

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Best Local Similarity
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                                AUTHORS
TITLE
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                   REFERENCE
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/clone="IMAGE:2491091"
/clone_lib="NCI_CGAP_Utl"
/tissue_type="well-differentiated endometrial
denocarcinoma, 7 pooled tumors"
/lab_host="Differentiated endometrial
/lab_host="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
a 155 c 134 g 158 t 3 others
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Eµkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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602998590F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5140583 5
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Pred. No. 3e-142;
0; Mismatches 3;
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Matches 622; Conservative
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/tissue_type="cervical carcinoma cell line"
/lab_host="0H10B"
/note="0rgan: cervix; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga.lln.gov. d column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 gtggaaaggaccatgctagactttccccagcatgtatccttgacaaagaagtacgagca 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 ACTGTGGCTGGCAGAAATGTTTTAAGATGGGATCTTTCACCAGAGCAAATTAAAACAAGA 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 gcaagtacagaagcagacaaaagactttctcgtttttgatattgagatgagcatgagagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 gatatatttgggagaattgttcatttacaggaaacctgtgatctggggaagataaaaacct
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                   1 (bases 1 to 789)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Pred. No. 1.5e-139;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5140583"
/clone_lib="NIH_MGC_12"
                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 33
High quality sequence stop: 789
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .789
                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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177 c
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99.0%;
                                                                                         Unpublished (1999)
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Seg primer: T3 POLYA-No.
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VERSION
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AUTHORS
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/db_xref="taxno" sapiens
/db_xref="taxno" s606"
/clone=_lib="NIH_MGE.4431130"
/tissue_type==adenocarcinoma, cell line"
/tissue_type=adenocarcinoma, cell line"
/tab_host="DH10B (phage-resistant)"
/note="toyan: prostate; vector: pcw-sporr6; site_1: NotI;
site_2: sall; cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 579)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
ltd.com/llnl.gov
Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1104 agaggaactcaagtattccatagaccaagagttcctcaaggaatacttcccaattgaggt 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1164 ggtcactgaaggettgetgaacacetaceaggagttgttgggaettteatttgaacaaat 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GGGTTTTGAATATGATGGGAAAATCAATGCCTGGGATCTATATTACTACATGACTCAGAC 69
                                                                                                                                                                            BG180236 579 bp mRNA EST 06-FEB-2001
602329846F1 NIH_MGC_91 Homo sapiens CDNA clone IMAGE:4431130
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                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                 1. .579
/organism="Homo sapiens"
                                                              601 gattttaacaaaaacctcaatgaggatgata 631
                                                                                                                                                                                                                                           BG180236.1 GI:12686939
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                                                                                                                                                                                                           mRNA sequence.
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KEYWORDS
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1 (bases 1 to 902)
Xiao, H.S., Han, Z.G., Zhang, F.X., Huang, Q.H., Lu, Y.J., Bao, L., Fu, G.,
Guo, C., Yan, Q., Jin, S.X., Zhu, Z.D., Xu, X.R., Li, N.G., Chen, Z. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG666754 902 bp mRNA EST 30-APR-2001
DRABUG01 Rat DRG Library Rattus norvegicus cDNA clone DRABUG01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                        1404 agtggcctccttggtgaacttctcacagccagtggcagtccctctctcctgag 1463
                                                                                                                                                                                                                                                                                                       1464 acacgacgaggtgaggacttactttcatgagtttggtcacgtgatgcatcagatttgtgc 1523
                                                                                                                                                                                                                                                                                                                                                                                                                   acagactgattttgcacgatttagcggaacaaatgtggaaactgactttgtagaggtgcc 1583
                                                                              1344 tgcggcctgcttcggtctccagcctggctgccttctgcctgatggaagccggatgatggc 1403
                                                                                                            110 TGGGCCTGCTTCGGTCTCCAGCCTGGCTTCTGCCTGATGGAAGCCGGATGATGGA 310
                                                                                                                                                                                                                        490 ACAGACTGATTTTGCACGATTTAGCGGAACAAATGTGGAAACTGACTTTGTAGAGGTGCC 549
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Distinct gene expression profiles of rat dorsal root ganglion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zhang Xu
Laboratory of Sensory System
Linstitute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-6471448700-121
Fax: 86-21-6471446
Bmail: xu.zhangëton.ac.cn
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    .902
    /organism="Rattus norvegicus"

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/db_xref="taxon:10116"
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/clone_lib="Rat DRG Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induced by peripheral nerve axotomy Unpublished (2001)
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238 c 239 g
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BG666754
BG666754.1 GI:13888661
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DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:

thttp://mage.llnl.gw.

http://mage.llnl.gw.

Plate: LLAMI175 row: f column: 13

High quality sequence start: 2

High quality sequence start: 2

High quality sequence story: 700.

Location/Qualifiers

1. 745

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/clone="IMAGE:564972"
/clone="IMAGE:564972"
/clone="IMAGE:564972"
/lab.bost="Hill® (TI phage-resistant)"
/lab.bost="Hill® (TI phage-resista
Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
Local Similarity 84.78;
les 619; Conservative
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

| | (bases 1 to 745)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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602908251F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5064972
5'; mRNA sequence.
BI144134
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                                                                                                                                                                                                                                                                                                                                                                                 61 AGGTGGTCACGGAAGGCTTGCTAAGCATCTACCAGGAGCTGCTGGGGACTTTCATTTGAAC 120
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                                                                      Length
                                                                                                                                Indels
                                                                   Score 506.8; DB 11;
Pred. No. 6.4e-114;
0; Mismatches 107;
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nilarity 84.2%;
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 Length 745;
                        Indels
Score 479.4; DB 11;
Pred. No. 3.3e-107;
1; Mismatches 102;
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Email: cgapbs-r@mail.nih.gov

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

BI144134 LOCUS

RESULT

ORGANISM

AUTHORS TITLE

JOURNAL COMMENT

REFERENCE

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                                                                                                                                                                   619 bp mRNA EST 07-SEP-2000
SOBIES_MOUSE_NMIE MUS MUSCULUS CDNA Clone IMAGE:2780253
to SW:NEUL_RAT P42676 NEUROLYSIN PRECURSOR ;, mRNA
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Other_ESTs: upsBall.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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1602 --ttgggtgtgggacgtcgattccctccgaa--gattgtcaaaacattataaagatggaa 1657
                   Gaps
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85.6%; Pred. No. 2.8e-106;
iive 0; Mismatches 89;
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/strain="C3H x 101 (F1 stock)"
/db_xref="taxon:10090"
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/clone_lib="Soares_mouse_NMIE"
/sex="male"
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/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 745)

S NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10428 row: o column: 06

High quality sequence stop: 698.
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/lab_host="DH10B (phage-resistant)"
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/clone_lib="NIH_MGC_92"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. II (bases 1 to 559)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 26-OCT-2000 musculus cDNA clone IMAGE:3483124
                                                                                                                                                                                                                                                         121 actytggctggcagaaatgttttaagatgggatctttcaccagagcaaattaaaacaaga 180
                                                                                                                                                                                                                                                                                                         gaggaagtaacttacgagaactgtctgcaggcactggcagatgtagaagtaaagtatata 300
                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                       511
                                                                                                                                                          ttactcagaatgacgttaggagagagagtgatgtctcctcttcaggcaatgtcttcctat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gatä-tatttgagagaattgttcattt--acaggaaacctgtgatctggggaagataaaa 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cctgaggccagacgatacttggaaaagtcaattaaaatggggaaaagaaatgggctccat 537
                                                                                                                                                                                                                           GAGGAAGTAACTTACGAGAACTGTCTGCAGGCACTGGCAGATGTAGAAGTAAAGTATATA 451
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                        gtggaaaggaccatgctagactttccccagcatgtatcctctgacaaagaagtacgagca
                                                                                                                                                                                                                                                                                                                                                                                                                   632 ACTGAGG-CAGACGATAC-TGGGAAAGTCAATTACAATGGGGGCAAAGAAATGGCGTCCAT
                                                                                                                                    7;
                                                                                                             DB 11; Length
                                                                                                                                    Indels
                                                                                                            Score 472.6; DB 11
Pred. No. 1.6e-105;
0; Mismatches 14;
                                                             166
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BE311015
                                                            210 g
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                                                                                                           / Match 22.3%;
Local Similarity 96.3%;
les 548; Conservative
                                                             166 c
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                                                                                                             Query Match
Best Local
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BE311015
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                    212
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AUTHORS
TITLE
JOURNAL
COMMENT
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggctgccctcgtggtgaacttctcacagccagtggcaggtcgtccctctctcctgagaca 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcaaatgcttgaaaattggggtgtgggacgtcgattccctccgaagattgtcaaaacatta 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1167 cactgaaggettgetgaacacetaceaggagttgttgggaettteatttgaacaaatgae 1226
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                                               þe
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                                               can
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Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM8513 row: p column: 05
High quality sequence stop: 557.
Location/Qualifiers
1. .559
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 559;
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 10;
.2e-101;
                                                                                                                                                                                                                                          tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                          /strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3483124"
/clone=lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross ti
/dev_stage="7" months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 455.6; E
Pred. No. 2.2e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     136 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 88.5
Matches 494; Conservative
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AW732454
AW732454.1 GI:7632786
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Matches 436; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
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AW732454
LOCUS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and "minmatch 12 options.

PCR PRIMERS

FORMARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 509)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
De Dox 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and an an an analysis of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1754 atcagtctcttcataccaacacatcgctggatgctgcaagtgaatatgccaaatactgct 1813
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                       AW786845 509 bp mRNA EST 01
120431 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW786845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 431.4; DB 10;
Pred. No. 2e-95;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 39 row: N column: 18
Seq primer: ATTTAGGTGACACTATAG.
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1...509
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91.7%;
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                                                                                                                                                                                              scrofa
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ORIGIN
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                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                              AUTHORS
4W786845
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Organism="Homo sapiens"

/organism="Homo sapiens"

/organism="Homo sapiens"

/clone="INAGE:2958628"

/clone=lib="NIH_MGC_14"

/clone=lib="NIH_MGC_14"

/clone=lib="NIH_MGC_14"

/clone=lib="NIH_MGC_14"

/clone=lib="NIH_MGC_14"

/clone=lib="NIH_MGC_14"

/clone="Corgan: Ridney; Vector: pOTB7; Site_1: XhoI; Site_2: BCORI; CDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit

/cliffornia, Berkeley) using ZAP-CDNA synthesis kit
/cliffornia, Berkeley) using ZAP-CDNA synthesis kit
/cliffornia long laborscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs rémail.nih.gov

Tissue Procurement: DcTp/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing

Found through the I.M.A.G.E. Consortium/LLNL at:

Image.llnl.gov/image/html/iresources.shtml

Seq primer: -40RP from Gibco

High quality sequence stop: 393.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 570)
1934 atatgttttacagctgttttaaaaaaaaagaaggataatgaatccagaggttggaatgaaat 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 511)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Sakon, R., Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mm42g01.yl Stratagene mouse melanoma (#937312) Mus musculus cDNA clone IMAGE:524208 5' similar to SW:NEUL_RAT P42676 NEUROLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Email: mousesext@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                       gcaagtacagaagcagacaaaagacttctcgttttgatattgagatgagcatgagagga 420
                                                                                                     345
121 actytygctygcagaaatytttaagatyggatctttcaccagagcaaattaaaacaaga 180
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                   actgaggageteattgtgcagaccaaacaggtgtacgatgetgttggaatgeteggtatt
                                                                                  /organism="Mus musculus"
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:524208"
/clone=lib=Stratagene mouse melanoma (#937312)"
/tissue_type="melanoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative full length read vector to vector length is 741 possible reversed clone: similarity on wrong strand Seq primer: -40RP from Gibco High quality sequence stop: 351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                               EST
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; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dr. From M2 cells, a highly metastatic derivative of the K-1735 (mouse) melanoma. Average insert size: 1.0 kb; Uni-2AP XR Vector; -5' adaptor sequence: 5' GAATTCGCACGG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 757) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                  511;
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                                                                                                                                                                                                    Score 416.8;
Pred. No. 7.6
                                                                                           -3' adaptor sequence:
115 c 134 g 122
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AW003054.1 GI:5849892
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88.4%;
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Unpublished (1997)
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FEATURES

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Score 376.8; DB 1
Pred. No. 5.3e-82;
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/db_xref="taxon:10116"
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158 c 127 g
   GI:13305246
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89.2%;
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Matches 405; Conservative
                                                                                                    Rattus norvegicus
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Best Local Similarity
   BG380774.1
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UI-R-CTO-bub-c-06-0-UI.S1 UI-R-CTO Rattus norvegicus cDNA clone
UI-R-CTO-bub-c-06-0-UI 3', mRNA sequence.
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                    CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1082 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 382.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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BASE COUNT ORIGIN

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Drogram for Rat Gene Discovery and Mapping
University of Lowa
University of Lowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mosores@blue.weeg.uiowa.edu
The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand connown and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
The following repetitive elements were found in this cDNA sequence:
1-36, >AT_rich#Low_complexity 84-105, >AT_rich#Low_complexity
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Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library constructed and normalized by Bento Soares and M.Fatima
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                             tggatatctttggagtgaagtattttccatggatatgttttacagctgttttaaaaaaga 1961
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                     440 TGGATATCTTTGGAGTGAAGTGTTTTCCATGGACATGTTTCACAGCTGTTTTAAAAAAGA
                                                      1962 agggataatgaatccagaggttggaatgaaatacagaaacctaatcctgaaacctggggg
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High quality sequence stop: 457
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 417)
Hillier, L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Ghellenberg, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA152501 417 bp mRNA EST 01-AUG-1997 2007a04 r.1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:566958 5, similar to SW:NEUL_RABIT P42675 NEUROLYSIN PRECURSOR;, mRNA sequence.
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                                                        94 ATGATCACCCTGTGCCTTTCGGCTCTGCGAGGCCTCCACAGAGCTGGTGGTTCCAGGATT 153
                                                                                                                                                                                                                                               atgatcgcccggtgccttttggctgtgcgaagcctccgcagagttggtggttccaggatt
                                                                                                                       61 ttactcagaatgacgttaggaagaagaagtgatgtctcctcttcaggcaatgtcttcctat
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   634 CAAAACACNTTATAANATGAATTNAAATAAATGAATAGAAAA 675
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AA152501.1 GI:1718695
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Std Error: 0.00
                           Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 315.
Location/Qualiflers
Insert Length: 2006
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Search completed: January 14, 2002, 19:34:07 Job time: 2176 sec

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423, App 3852, Ap 3852, Ap 3854, Ap 3855, Ap 3856, Ap 3860, Ap 3861, Ap 3862, Ap 3862, Ap 3862, Ap 3864, Ap 3864, Ap 3866, Ap

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Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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709 gacaagtataaaattaccttaaaatatccacactatttccctgtcatgaagaaatgttgt 768
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 18292, Application US/09933524A

GENERAL INFORMATION:
APPLICANT: Dananc, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Date, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Jones, Lee W.
ITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
ITLE OF INVENTION: From Various Libraries
FILE REPERENCE: 774
CURRENT APPLICATION NUMBER: US/09/933,524A
CURRENT FILING DATE: 2001-08-20
PRIOR PAPLICATION NUMBER: 09/528,409
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: HY-Patent.pl Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.6%; Score 371.8; DB 6; 98.9%; Pred. No. 8.4e-90; tive 1; Mismatches 3;
US-09-806-866-54
US-09-806-866-60
US-09-897-516-3852
US-09-897-516-3853
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US-09-897-516-3868
                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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Matches 373; Conservative
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ORGANISM: Homo sapiens
  US-09-933-524A-18292
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  LENGTH: 408
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                                                                                             ; Search time 380.46 Seconds (without alignments) 10766.075 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56, Appl
50, Appl
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Compugen Ltd.
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US-09-826-734-43

US-09-938-27547

US-09-939-397-39435

US-09-939-397-39669

US-09-939-397-39669

US-09-939-354A-365

US-09-938-374A-365

US-09-938-54A-365

US-09-938-54A-365

US-09-938-54A-365

US-09-985-743A-149

US-09-885-439A-5148

US-09-885-439A-516-2237

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US-09-897-516-2242

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            GenCore version
Copyright (c) 1993 - 2000
                                                                                               January 14, 2002, 19:34:11
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Maximum Match 100%
Listing first 45 summaries
                                                                  nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Length 408;

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Score

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GENERAL INFORMATION:
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APPLICANT: Vernet, Corine A.M.
APPLICANT: Vernet, Corine A.M.
APPLICANT: Waihra, Vishnu S.
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Schusen, Bryan D.
APPLICANT: Rekuda, Ramesha
TITLE OF INVENTION: NOVel Polynucleotides and Polypeptides Encoded Thereby
FILE REFERENCE: 15966-754
CURRENT APPLICATION NUMBER: US/09/826,734
CURRENT FILING DATE: 2001-04-05
PRIOR PPLICATION NUMBER: 60/195,576
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 270
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 22/2
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                  1009 attitgaatttgaagaaaaggaatgcaaagacaggggttttgaatatgatgggaatc 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: | MAME/KRI: | MISC_feature | LOCATION: (0)...(0) | OTHER INFORMATION: Expressed in placenta | DCATION: (0)...(0) | OTHER INFORMATION: Expressed in placenta | LOCATION: (0)...(0) | OTHER INFORMATION: correct | LOCATION: (0)...(0) | OTHER INFORMATION: correct | LOCATION: (0)...(0) | OTHER INFORMATION: correct | LOCATION: (0)...(0) | OTHER INFORMATION: Encodes protein in sequence listing 44 that is 97% | OTHER INFORMATION: similar to gill783127| endopeptidase 24.16 type | US-09-826-734-43
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                                                                                                                                                                                                                 Sequence 43, Application US/09826734 GENERAL INFORMATION:
                                                                                        1069 aatgcctgggatctata 1085
                                                                                                                         392 aatgeetgggatetata 408
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Matches 216; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-898-888A-27547
                                                                                                                                                                                                US-09-826-734-43/c
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1743 gagcaaagttgatcagtctcttcataccaacacatcgctggatgctgcaagtgaatatgc 1802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 gctgctgcggatgtcgcggcactaccgcacaggcagcgccgtgcccgggagctcctgga 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 cgccaaggtggaccaggcctgcacacgcagacgagacgcagacccgccgaggagtatgc 301
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TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748CON1
CURRENT APPLICATION NUMBER: US/09/898,888A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR APPLICATION NUMBER: US 09/205,070
PRIOR FILING DATE: 1999-06-28
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27547
LENGTH: 543
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Pred. No. 4e-45;
0; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11054, Application US/09933524A; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or .
US-09-898-888A-27547
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PPLICANT: Labar, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%;
62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 62.8
Matches 333; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                        Length 449;
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GENERAL INFORMATION:

APPLICANT: Hyseq. Inc.

TITLE OF INVERNION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVERNION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVERNION: NOVER: 2041-765

CURRENT APPLICATION NUMBER: US/09/339,397

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 09/289,768

PRIOR APPLICATION NUMBER: 09/289,768

PRIOR APPLICATION NUMBER: 09/289,768

NUMBER OF SEQ ID NOS: 39996

SOFTWARE: FastEEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                               Indels
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 774
                                                                                                                                                                                                                                                                                                                    Score 190.2; DB 6;
Pred. No. 6.5e-41;
0; Mismatches 158;
                                                       CURRENT APPLICATION NUMBER: US/09/933,524A CURRENT FILING DATE: 2001-08-20 PRIOR APPLICATION NUMBER: 09/528,409 PRIOR FILING DATE: 2000-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1780 ctggatgctgcaagtgaatatgc 1802
                                                                                                                                    NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 11054
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
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SEQ ID NO 39435
LENGTH: 479
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                                                                                                                                                                                                                                                                                                                                             1565 ctgactttgtagaggtgccatcgcaaatgcttgaaaattgggtgtgggacgtcgattccc 1624
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                                                                                                                                                                                                                                                                                            48 atgggagccgacagatcgccatcgcggccatggtggccaacttcaccaagcccacagccg 107
                                                                                                                                                                                                                                                                                                                                                                                           108 acgogecetcgctgctgcagcatgacgaggtggagacctacttccatgagtttggccacg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 tgctgcggatgtcgcggcactaccgcacaggcagcgccgtgtcccgggagctcctggaga 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 agctcattgagtcccggcaggccaacacaggcctcttcaacctgcgccagatcgtcctcg
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                                                                                                                                               Length 479;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILL REFERENCE: 20411-765
CURRENT APPLICATION NUMBER: US/09/939,397
CURRENT APPLICATION NUMBER: 09/289,768
PRIOR APPLICATION NUMBER: 09/289,768
                                                                                                                                          Query Match 8.4%; Score 176.8; DB 5; Best Local Similarity 63.3%; Pred. No. 2.7e-37; Matches 271; Conservative 0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 6.0%; Score 126; DB 5; Similarity 66.7%; Pred. No. 1.2e-23; 30; Conservative 0; Mismatches 90
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39669
LENGTH: 471
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US-09-939-397-39669
; NAME/KEY: misc_feature
; LOCATION: (1)...(479)
: CTHER INFORMATION: n = A,T,C or
US-09-939-397-39435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaccatgctagactttccccagcatgtatcctctgacaaagaagtacgagcagcaagta 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctggcagaaatgttttaagatgggatctttcaccagagcaaattaaaacaagaactgagg 187
           150 coccaggaaccaacgtgcctgcaaccttcggccatctggcaggtggctaccacgcccagt 209
                                                                       210 actacgggtacctgtggagcgaggtgtattccatggacatgttccacacgcgcttcaagc 269
                                                                                                                                                                                              330 goggitccgaggatgccagcgccatgctgaggcgcttcctgggccgtgaccccaagcagg 389
                                            270 aggalggtgtcctgaacagcaaggttggcatggattacagaagctgcatcctgagacccg
                                                                                                          1958 aagaagggataatgaatccagaggttggaatgaaatacagaaacctaatcctgaaacctg
5.8%; Score 121.8; DB 6; Length 468; 64.2%; Pred. No. 1.7e-22; tive 0; Mismatches 102; Indels 0
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
ITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
ITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/933,524A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 7235
LENGTH: 468
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; OTHER INFORMATION: n = A,T,C or
US-09-933-524A-7235
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Best Local Similarity
Matches 183; Conserv
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Sequence 3065, Application US/09933524A
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/933,524A
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 09/528,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; DB 6;
3e-16;
                                                                                        APPLICANT: Shenk, Michael Andrew TITLE OF INVENTION: Polynucleotides Isolate TITLE OF INVENTION: Methods For Their Use FILE REFERENCE: 11000.1013U CURRENT APPLICATION NUMBER: US/09/388,906A CURRENT FILING DATE: 1999-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 98.6;
Pred. No. 3e
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 24843
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20678
                                   Sequence 20678, Application US/09388906A GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka
APPLICANT: Shenk, Michael Andrew
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milarity 52.0%; 1
Conservative 0,
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US-09-388-906A-20678
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Best Local Similarity
Matches 244; Conserv
RESULT 8
US-09-388-906A-20678
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TYPE: DNA
ORGANISM: Zea mays
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Best Local S
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: LIBBARIES
FILE REFERENCE: 20411-748CON1
CURRENT APPLICATION NUMBER: US/09/898,888A
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-106-28
PRIOR SPELICATION NUMBER: US/09/340,623
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FASSEQ for Windows Version 3.0
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Pred. No. 2.8e-15;
0; Mismatches 87; Indels
                                                                                                                                                                                              Score 96.2; DB 6;
Pred. No. 1.2e-15;
0; Mismatches 88;
                                                                                                                                                                                                                                     0; Mismatches
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 3065
LENGTH: 391
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4.5%;
Best Local Similarity 62.8%;
Matches 147; Conservative
                                                                                                                                                                                              Query Match 4.5%;
Best Local Similarity 62.9%;
                                                                                                                                                                                                                                   Matches 149; Conservative
                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-09-933-524A-3065
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ORGANISM: Homo sapiens
US-09-898-888A-37608
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US-09-898-888A-37608
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM A CDNA LIBRARY OF HUMAN BONE MARROW AND HUMAN FETAL
TITLE OF INVENTION: PROM A CDNA LIBRARY OF HUMAN BONE MARROW AND HUMAN FILE REFERENCE: 20411-731CON1
CURRENT APPLICATION NUMBER: US/09/927,875A
CURRENT APPLICATION NUMBER: 09/713,841
PRIOR PILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 13540
SOFTWARE: PEASLEG for Windows Version 3.0
SEQ ID NO 9719
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APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/839,976A
CURRENT APPLICATION NUMBER: 02/294,093
PRIOR APPLICATION NUMBER: 09/294,093
PRIOR FILING DATE: 1999-04-16
SEQ ID NOS: 6207
SOFTWARE: PERL PROGRAM
SEQ ID NO 149
LENGTH: 270
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Pred. No. 1.8e-13;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94.8; DB 6;
Pred. No. 2.8e-15;
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; OTHER INFORMATION: Incyte ID No: 700342237H1
US-09-839-976A-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
Sequence 9719, Application US/09927875A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 149, Application US/09839976A GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.2%;
58.1%;
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Best Local Similarity 62.8%;
Matches 147; Conservative
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Matches 155; Conservative
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1753 gatcagtctcttcatacca 1771
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Best Local Similarity 52.55
Matches 199; Conservative
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NAME/KEY: unsure
LOCATION: (1)..(637)
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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1145 aatactteeeaattgaggtggteactgaaggettgetgaacacetaeeaggagttgttgg 1204
                                                                      1205 gactitcatitgaacaaatgacagatgcicatgtitggaacaagagtgitacactitata 1264
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Sequence 44048, Application US/09985678
GENERAL INFORMATION:
APPLICANT: Cheath, Nordine
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 16517.255/38-21(15097)F
CURRENT FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 44448
LENGTH: 269
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APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
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Matches 154; Conserv
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; ORGANISM: Zea mays
US-09-985-678-44048
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US-09-865-439A-67646
US-09-865-439A-67646
US-09-865-439A-67646
Sequence 67646, Application US/09865439A
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51936)B
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 67646
APPLICANT: La Rosa, Thomas J.

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51936)B
FILE REFERENCE: 38-21(51936)B
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 20408
LENGTH: 2513
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Pred. No. 7.3e-11;
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                                                                     Query Match 3.7%; Score 78.2; DB 5; Length 637; Best Local Similarity 52.2%; Pred. No. 1e-10; Matches 198; Conservative 0; Mismatches 178; Indels
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3587-284-Q1-K6-C10
US-09-865-439A-67646
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Search completed: January 14, 2002, 21:26:15 Job time: 6724 sec

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; TOPOLOGY: linear
MOLECULE TYPE: protein
; FRAGNENT TYPE: N-terminal
PCT-US92-00731-13
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Best Local Similarity 86.79
Matches 568; Conservative
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(without alignments)
855.417 Million cell updates/sec
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2: /cgn2_6/ptcdate/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdate/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdate/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdate/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdate/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-07-977-434-12
US-08-128-142-2
US-09-128-142-2
US-09-128-142-4
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US-08-128-142-4
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US-08-993-47
US-08-993-299-11
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US-08-933-992-29
US-09-308-375-2
US-09-308-29-11
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Maximum DB seq length: 2000000000
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Sequence 24, Appli Sequence 2, Appli Sequence 6, Appli Sequence 12, Appli	# 1.25
PCT-US94-10261A-2 US-08-685-871-2 US-08-973-462-8 US-08-973-462-8 US-08-973-462-8 US-08-973-462-9 US-08-100-178-2 US-08-995-654-2 US-08-995-654-2 US-08-997-65-6 US-08-973-922A-6 US-08-915A-6	GNMENTS OOFEFTIDAS 731 731 7415 PC
1713 1354 1786 1786 422 422 422 422 422 422 422 1351 1351 126 476 476 475 475 475 475 1126 1126 1126 1126 1169 4169	RESULT 1 PCT-US92-00731-13 Sequence 13, Application PC/TUS920073 GENERAL INFORMATION: APPLICANT: Kawabata, Shunichiro TTYLE OF INVENTION: MICKOSOMAL EN TITLE OF INVENTION: MICKOSOMAL EN TITLE OF INVENTION: MICKOSOMAL EN TITLE OF INVENTION: MICKOSOMAL EN NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: STREET: 6300 Columbia Center CITY: Seattle STATE: Washington COUNTRY: US ZIP: 98104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ISBN CCOMPATA: MEDIUM TYPE: Floppy disk COMPUTER: ISBN CCOMPATA: MEDIUM TYPE: Patentin Release #1.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US92/00 FILING DATE: 19920128 CLASSIFCATION: 435 CLASSIFCATION: 435 PRIOR APPLICATION NUMBER: US 07/646,99 FILING DATE: 19920128 CLASSIFRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 31,393 REPRENCE/DOCKET NUMBER:
	T. 1 S92-00731-13 BS92-00731-13 BERGEL INFORMATION: APPLICANT: Kawabata, Shu APPLICANT: Kawabata, Shu APPLICANT: Bavie, Earl W TITLE OF INVENTION: MICE NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: 13 CORRESPONDENCE Sed and Be: STREET: 6300 Columbia (ITY: Seartle STREET: 6300 Columbia (COUNTRY: US ZIP: 98104 COMPUTER: Deathington COUNTRY: US ZIP: 98104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di. COMPUTER: DEATHING POPERATION DATA: APPLICATION NUMBER: PC FILING DATE: 19920128 CLASSIFICATION NUMBER: US FILING DATE: 28-JAN-19 RECISTRATION NUMBER: US RECISTRATION NUMBER: US RECISTRATION NUMBER: US TELECOMMUNICATION INFORMATION NAME: MAKI, DAVIG J TELETX: 3723836 TELETX: 3723836 TELETX: 3723836 TELETX: 3723836 TELENX: TOO amino acid TYPE: AMINO ACID
111.5 111.1 111.1 111.1 110.5 110.5 110.5 100.5	ULT 1 -US92-00731-13 GENERAL INFORMATION FAN APPLICANT: KAN APPLICANT: KAN APPLICANT: TAN TITLE OF INVENT UMBER OF SEQUI CORRESPONDENCE ADDRESSEE: 630 CITY: SCALL COUNTRY: US ZIRET: 03104 COUNTRY: US ZIRET: BADDL COUNTRY: US ZIRET: GAN COUNTRY: US ZIRET: GAN COUNTRY: US
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Length 709; Indels

81.2%; Score 2979; DB 5; 86.7%; Pred. No. 4.6e-264; Live 29; Mismatches 56; ~

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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                               HYYMTQTEELKYSIDQEFIKEYXPXXXGGXXRGLNIYQELLGLXFEQVADAHVWNPXVT 473
                                                                                                                                                                                                                                                                                                                                                                                 VAGRPSLLRHDEVRTYFHEFGHVMHOICAQTDFARFSGTNVETDFVEVPSQMLENWVWDV 539
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                                                                                                                                                      YYYMTQTEELKYSIDQEFLKEYFPIEV--VTEGLLNTYQELLGLSFEQMTDAHVWNKSVT 419
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             62 EELİVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRAA 121
                                                                                             122 STEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHLP 181
61
                                                                                                          EQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sinha, Sukanto
APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: McConloque, Lisa C.
APPLICANT: Johnstone, Edward M.
APPLICANT: Johnstone, Edward M.
APPLICANT: MRY SOURNES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Athena Neurosciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Athena Neurosciences, Inc. STREET: 800F Gateway Blvd. CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/766,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/07766351; Patent No. 5292652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              Length 689;
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                                                                                                                                                                                                                                                                                                                                                                               98; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                            63.5%; Score 2331; DB 1;
64.9%; Pred. No. 9.5e-205;
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTDHY, Lisabeth Feix
REGISTRATION NUMBER: 3147
REFERENCE/DOCKET NUMBER: 17796-002
TELEPHONE: (415) 877-0900
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-0900
TELEFAX: (415) 877-0910
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENTH: 689 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 5, Application US/08059032 ; Patent No. 5424205
                                                                                                                                                                                                                                                                                                                                              Query Match 63.59
Best Local Similarity 64.99
Matches 426; Conservative
                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: prof
                                                                                                                                                                                                                                                      ; HYPOTHETICAL: N; ANTI-SENSE: NO US-07-766-351-5
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382 HHEEGASAWHEDVRLYTARDAASGEVVGKFYLDLYPREGKYGHAACFGLQPGCLRQDGSR 441
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                                                                                                                                    QSLHTNTSLDAASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMD
                                                                                                                                                                                                                                                                       646 MFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGL 701
                                                                                                                                                                                                                                                                                         APPLICANT: Little, Shella P.
APPLICANT: Johnstone, Edvard M.
TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07290
FILING DATE: 19911004
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Athena Neurosciences, Inc. STREET: 800F Gateway Blvd. CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murphy, Lisabeth Feix
REGISTRATION NUMBER: 31547
REFERENCE/DOCKET NUMBER: 17796-002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               PCT-US91-07290-5; Sequence 5, Application PC/TUS9107290; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sinha, Sukanto
APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: McConlogue, Lisa C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 877-0900 TELEFAX: (415) 877-8370 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 689 amino acids TYPE: AMINO ACID
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Matches 426; Conservative
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MEDIUM TYPE: Floppy
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PCT-US91-07290-5
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 APPLICANT: Seubert, Peter A.
APPLICANT: Dovey, Harry F.
APPLICANT: McConlogue, Lisa C.
APPLICANT: Little, Sheila P.
APPLICANT: Johnstone, Edward M.
TITLE OF INSURION: Amyloidin Protease and Uses Thereof
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower, STREET: Suite 2000
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, William E.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEFRAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 689 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/059,032
FILING DATE: 19930507
Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 426; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 199305
CLASSIFICATION: 435
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US-08-059-032-5
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             DFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLP 285
                                                                                                                                                                                                     KDRGFEYDGKINAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSF 405
                                                                                                                                                                                                                                                                     EVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVD 585
                                                                                                                                                                                                                                                                                                                                                                         LDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRY
                                                 LEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPD
                                                                                                                 LRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKEC
                                                                                                                                                                 EQMIDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSR
                                                                                                                                                                                                                                                                                                         466 MMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GS-08-353-700+1
Sequence 1, Application US/08353700
Sequence 1, Application US/08353700
Parent NO. 5599919
SERVERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATNER, JEROME B.
TITLE OF; INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF; INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF; INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: DANN, DORFMAN, HERRELL AND SKILLMAN 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/353,700 FILMGPDATE: 09-DEC-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: REED, JANET E. REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 563-4100
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APPLICANT: Ratther, Jerome B.
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 RAEQAFQASQIKENELRRSMEEMKKENNLLKS--HSEQ------KAREVCHLEAELK 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 VVTEGLINTYQEL---LGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 KYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMH 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 OMKARLTQELQQAKNMH-------NVLQAELDKLTSVKQQLENNLEEFKQKLC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91; Mismatches 238; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3248;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505 QICAQTDFARFSGINVETDFVEVPSQMLENWVWDVDSLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 122; DB 1;
19.8%; Pred. No. 0.22;
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                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
(215) 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 19.8
Matches 116; Conservative
                                                                                                                                               single
                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                   amino acid
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                                                                                                             TYPE: amino aci
STRANDEDNESS: S
TOPOLOGY: lines
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ANTI-SENSE: N
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554 PIADDLLEKLVASRLVNTGLL--TLRQIVLSKVDQSLHTNTSLDAAS
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FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20 NOV-1995
PRIOR APPLICATION DATA:
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7.08-685-576-1
7. Sequence 1, Application US/08685576
8. Parkent No. 5906819
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 1388 amino acids
                                                                                                                                                                                                                                          APPLICANT: Kaibuchi, Kozo
APPLICANT: Iwamatsu, Akihii
APPLICANT: Nakano, Takeshi
APPLICANT: Ito, Masaaki
APPLICANT: Takahashi, No.
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TELEFAX: (202)672-5399
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Matches 79; Conserve
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CITY: Washington
STATE: D.C.
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ZIP: 20007-5109
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803 EQGSMP--SERSECRLEADQSPKNSAILQN---RVDSLEFSLESQKQMNSDLQKQCEELV 857
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                                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.3%; Score 122;
19.8%; Pred. No. 0
                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                COMPUTER: IBM PC' compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3248 amino acids
                                                                                              MEDIUM TYPE: Floppy disk
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Matches 116; Conservative
                                        ZIP: 19103-2307
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not
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                                                                                                                                                                                                                                                FILING DATE
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PCT-US95-16216-1
STATE: Pi
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53 SPEQIKTRTEELIVQTKQVYDAVGML-GIEE-VTYENCLQALADVEVKYIVERTMLDFPQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 HVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEK-- 168
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                                  629 SERRDRTHGSEII-----NDLQGRISGLEEDVKNGKILLAKVELEKRQLQER----- 675
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No. 0.084; Conservative 83; Mismatches 158;
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3000 K Street, N.W., Suite 500
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721 IYESİLEEAKSEAMKEMEKKLSEERTLKQKVENLLLEAEKRCSILDCDLKQSQQKI----N 776
                               DFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRMEMAFNT-----RCKEENTII 279
                                                                                             LQQULPLRTKVAKLLGYSTHAD----FVLEMNTAKST---SRVTAFLDDLSQKLKPL 329
                                                                                                                             835 LEMKMSLEKQNAELRKERQDADGQMKELQDQLEAEQYFSTLYKTQVRELKEECEEKTKLC
                                                          ELLKOKDVLNEDVRNLTLKIEQ - - ETQKRCLTQNDLKMQTQQVNTLKMSEKQLKQENNHL
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONCLEASE MUTATIONS OF TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                            390 TEGLLNTYQ--ELLGLSFEQMTDAHVWNKSVTLYTVKD 425
                                                                                                                                                                                                                                                 941 KEKIMKELEIKEMMARHKQELTE----KDATIASLEE 973
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ADDRESSEE: Hoffmann-La Roche Inc.
STREET 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
PRILICATION NITWO
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                  US 590,466
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FILING DATE: 28-SEP-1990
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22-AUG-1986
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APPLICATION NUMBER: WO PC
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-SEP-1990 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 7.
FILING DATE: 15-AUG-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: |Nutley
STATE: | New Jersey
ZIP: 07110-1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gelfan
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397 YQELLGLSFEQMTD-----AHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VW-DVDSLRRLSKHYKDGSPIADDLLEKL --VASRLVNTGLLT-LRQIVLSKVDQSLHTN 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 MRGD-IFERIVHLQETCD-LGKIKPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------PE-----QFKDYLSLVGDQIDNIPGVKGIGKKTAVSLLKKYNSLE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 DFVLEMNTAKSTSRVTAFLDDLSQKLK---PLGEAEREFILNLKKKECKDRGFEYDGKIN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 NVLKNINLL--TEKLRRLLEDSKEDLQKSIELVELIYDVPMDVEKDEIIYRGYNPDKLLK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----FPIEVVTEGLLNT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 VLKKYEFSSIIKEL--NLQEKLEKEYILVDNEDKLKKLABEIEKYKTFSIDTETTSLDPF 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GSRMMAVAALVVNFSQPVAG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 YENCLQALADVEVKYIVERTMLDFPQHVSSDKEV-----RAASTEADKRLSRFDIEMS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 FPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQL-----LPLRTKVAKLLGYSTHA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 STPDLLLEQIPYVEELVDALG-----IKVLKIEGF----EADDIIATLSKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 SELCIDENKNLNEDDTFLVFSKAELGALPDD--FIDSLEK--TD---DDKYKITLKYPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | : | : | : | : | : | 31 HINAVYGLIKMLIKFLKE------HISIGKDACVFVLDSKGGSKKRKDILETYKANRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Score 116; DB 1; Length 892; 19.2%; Pred. No. 0.095;
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                                                                                                                                                                                                                                                                                         Case No. 5466591 8753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.2%; Score 116; DB Best Local Similarity 19.2%; Pred. No. 0.099 Matches 118; Conservative 113; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 AWDLYYYMTQTEELKYSIDQEFLKEY-----
                                                               PELLING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY AGENT INFORMATION:
NAME: Luann CSETE
                                            JMBER: US 455,611
22-DEC-1989
                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,822
20-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                              : 892 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-07-977-434-12
                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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Sequence 12, Application US/08458819
Patent No. 5795762
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA: WO PCT/US90/07641
APPLICATION NUMBER: WO PCT/US90/07641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/458,819
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
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APPLICATION DATE: 377,434
FILING DATE: 23-FEB-1993
APPLICATION NUMBER: 07/977,434
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: 0S 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 0S 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   E: Hoffmann-La Roche Inc
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 063,509 FILING DATE: 17-JUN-1987
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
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                                                                                                                                                                                                                                                                                                   STREET: 340 Kingsland Stree
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 2.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann
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RESULT 9
US-08-458-819-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 NVLKNINLL--TEKLRRLLEDSKEDLQKSIELVELIYDVPMDVEKDEIIYRGYNPDKLLK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 AWDLYYYMIQTEELKYSIDQEFLKEY--------FPIEVVTEGLLNT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 YQELLGLSFEQMTD-----AHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 --ACFGLQPG------CLLPD------GSRMMAVAALVVNFSQPVAG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 NDFSYVPLERAVEYSCEDADVTYRIFRKLGRKIYENEMEKLFYEIEMPLIDVLSEMELNG 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 MRGD-IFERIVHLQETCD-LGKIKPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 DFVLEMNTAKSTSRVTAFLDDLSQKLK---PLGEAEREFILNLKKKECKDRGFEYDGKIN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 VW-DVDSLRRLSKHYKDGSPIADDLLEKL--VASRLVNTGLLT-LRQIVLSKVDQSLHTN 591
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                                                                                                                                                                                                                                                                                                                                                                                                                   : | : | : | : | : | 31 HTNAVYGLTKMLIKFLKE------HISIGKDACVFVLDSKGGSKKRKDILETYKANRP 82
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                                                                                                                                                                                                                                                           Query Match 3.2%; Score 116; DB 1; Length 892; Best Local Similarity 19.2%; Pred. No. 0.095; Matches 118; Conservative 113; Mismatches 229; Indels 1
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PCT-US91-07055-12
; Sequence 12. Application PC/TUS9107035
; GENERAL INFORMATION:
    APPLICANT: Gelfand, David H.
    APPLICANT: Abramson, Richard D.
    TITLE OF INVENTION: 7 TO 3' EXONUCLEASE MUTATIONS OF TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
    NUMBER OF SEQUENCES: 38
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Getus Corporation
    STREET: 1400 Fifty-third Street
    CITY: Emeryville
    STATE: California
    ZIP: 94608
   12:
                                                            892 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 TSLDAASEYAKYCSEI 607
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                              protein
                                                                                    amino acid
                                                                                                                                           MOLECULE TYPE:
                                                                                                                TOPOLOGY:
                                                                                                                                                                         US-08-458-819-12
                                                            LENGTH:
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Sequence 2, Application US/09128142
Sequence 2, Application US/09128142
Patent No. 6294559
GENERAL INFORMATION:
APPLICANT: Smith, Roy G.
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMAI AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 FPVMKKCCIPETRRRMENAFNTRCKEENTIILQQL-----LPLRTKVAKLLGYSTHA 300
                                                                                                                                                                                                                                                                                                               358 AWDLYYYMTQTEELKYSIDQEFLKEY---------FPIEVVTEGLLNT 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                            333 EAKLVGISISTMEGKAYYIPVSHFGAKNISKSLI-DKFLKQILQEKDYNIVGQNLKFDYE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 -- ACFGLQPG------CLLPD------GSRMMAVAALVVNFSQPVAG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 RP-SLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGT-----NVETDFVEVPSQMLENW 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 VW-DVDSLRRLSKHYKDGSPIADDLLEKL--VASRLVNTGLLT-LRQIVLSKVDQSLHTN 591
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                                                                                                                                                                                                                            301 DFVLEMNTAKSTSRVTAFLDDLSQKLK---PLGEAEREFILNLKKKECKDRGFEYDGKIN 357
                                            196 SELCIDFNKNLNEDDTFLVFSKAELGALPDD--FIDSLEK--TD---DDKYKITLKYPHY
                                                                                     126 ES---DFEK-----VNIITGDKDLLQLVSDKVFVWRVERGIIDLVLYDRNKVIEKYGIY
                                                                                                                                                                                177 -----PE-----OFKDYLSLVGDQIDNIPGVKGIGKKTAVSLLKKYNSLE
                                                                                                                                                                                                                                                                        217 NVLKNINLL - - TEKLRRLLEDSKEDLOKSIELVELIYDVPMDVEKDEIIYRGYNPDKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: Power Macintosh 7500/100
SOFTWARE: Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Jack L. Tribble
STREET: 126 E. Lincoln Ave., P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,633
REGISTRATION NUMBER: 32,633
TELECOMMUNICATION INFORMATION:
TELECHONE: (908) 594-5321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,142
FILING DATE: 03-Aug-1998
CLASSIFICATION: <UNKnown>
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PRPLICATION NUMBER: 08/844,007
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 TATGKFSTNAEVLEEL 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 HTNAVYGLTKMLIKFLKE-----HISIGKDACVFVLDSKGGSKKRKDILETYKANRP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.2%; Score 116; DB 5; Length 892;
19.2%; Pred. No. 0.095;
tive 113; Mismatches 229; Indels 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stacey R. SEGISTRATION UNBER: 32,630 REFERENCE/DOCKET NUMBER: Case No. 2580 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US90/07641 FILLING DATE: 21-DEC-1990
                                                                                                               SUFTRACE.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07035
FTT.ING DATE: 19910930
                                                                                                                                                                      FILING DATE: 19910930
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING PAPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NIME.
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12-JAN-1988
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
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24-JUL-1990
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 59 FILING DATE: 28-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 45
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PRIOR APPLICATION DATA:
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AMINO ACID
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-AUG-PRIOR APPLICATION DATA:
             COMPUTER READABLE FORM:
MEDIUM | TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 12-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match,
Best Local Similarity
Matches 118; Conserv
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PCT-US91-07035-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 RAASTEADKRLSRFDIEMSMRGD------IFERIVHLQ---ETCDLG-K 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 KFKHITP-----LQEQSKEVAIRIFQGCQFRSVEAVQEI----TEYAKSIPGFVNLDLN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 DOVTLLKYGVH------EIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKP 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 QALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYK 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 IKPEARR----YLEKSIKMG-KRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.1%; Score 115; DB 4; Length 505; 20.5%; Pred. No. 0.047; ive 63; Mismatches 159; Indels 162;
                                                                                                                                                                                                                                        <Unknown>
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,142
FILING DATE: 03-Aug-1998
CLASSIFICATION: <UNKNOWN>
                                                                 PRIOR APPLICATION: ...

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,007
FILING DATE: GUNROON>
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/POCKET NUMBER: CURKNOT
TELEPHONE: (908) 594-5321
TELEPHONE: (908) 594-5321
TELEPHONE: (908) 594-5321
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
SOFTWARE: Microsoft Word 6.0
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US-08-766-014-2
; Sequence 2, Application US/08766014
; Patent No. 5744312
; PATENT INFORMATION:
APPLICANT: Mamone, Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.1%
Best Local Similarity 20.5%
Matches 99; Conservative
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Patent No. 6294559
GENERAL INFORMATION:
APPLICANT: Smith, Roy G.
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMAI AND GAMM
                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                59 TRTEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEV 118
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                       56 TRIDPVVADYK--YD----LKLQE--YQSAIK-VEPASPPYYSEKIQLYNKPHEEPSNSL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                      RAASTEADKRLSRFDIEMSMRGD-------IFERIVHLQ---ETCDLG-K 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ECKDRGFEYDGKINAWDLYYYMTQTEELKYSI-----DQEFLKEYFPIEVVTEGLL 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 IKPEARR-----YLEKSIKMG-KRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDT
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                                                                                                                                                                                                                                                          Query Match 3.1%; Score 115; DB 4; Length 477; Best Local Similarity 20.5%; Pred. No. 0.043; Matches 99; Conservative 63; Mismatches 159; Indels 162;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Power Macintosh 7500/100
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ADDRESSEE: Jack L. Tribble
STREET: 126 E. Lincoln Ave., P.O. Box 2000
CITY: Rahway
                                                                                 STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-128-142-2
TELEFAX: (908) 594-4720
                                                            LENGTH: 477 amino acids
                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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US-09-128-142-4
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393 ----YLLNPSESNYDLDR-VLKKYLKVDVPSYEGIFGKGRDKKKIEEIDENILADYJCS 446
                                                                   416 KSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVN 475
                                                                                                            -----LMNFIEEMDMKKLLLE 473
                                                                                                                                                             534
                                                                                                                                                                                                                                                      535 ------WWDVDSLRRLS------KHYKDGSPIADDLLEKLVASRLV 569
                                                                                                                                                                                                                                                                                508 IGEILDKIYKEAGYQFNVNSPKQLSEFLFEKLNLPVIKKTKTGYSTDSEVLEQLVPYNDI 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                             476 FSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLEN-
                                                                                                                                                                                            ----SGFTLDKEVLKELSQKIDDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.1%; Score 113.5; DB 2; Length 643;
Best Local Similarity 19.4%; Pred. No. 0.095;
Matches 86; Conservative 57; Mismatches 152; Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCENERARE: Patentin Ralease #1.0, Version #1.25 SCHRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511 FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAY 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/08245511
Patent No. 928900
GENERAL INFORMATION:
APPLICANT: Masure, H Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Klauber & Jackson
: 411 Hackensack Avenue
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                 447 RCVYLFDLKEK------
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568 VSDIIEYRQLTKLK 581
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 WDLYYYMTQTEELKYSIDQEFLKEYFPIEVVT-EGLLNTYQELLGLS--FEQMTDAHVWN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 PEQIKTRIEELIVQTKQVYDAVGMLGIEEVTYE----NCLQALAD---VEVKYIV-ERT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 MLDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERI-VHLQETCDLGKIKPEAR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- IDFN----KNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYKITLKYPHYFP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match, 3.1%; Score 115; DB 1; Length 872; Best Local Similarity 17.6%; Pred. No. 0.11; Matches 108; Conservative 115; Mismatches 195; Indels 196; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 DNIPGVPNIGEKTAIKLLKDFGTIENLIQNLSQLKGKIKENIENNKELAIMSKRLATIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 DIPIEIDFEEYKVKKPNEEKLLELFNKLEFFSL---IDNIKKESS-----
                          APPLICANT: Sha, Dan
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,688
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,014
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               December 15, 1995
                                                                                                                      ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 RYLEKSIKMGKRNGLHL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: December 15
ATTORNEY/AGENT INFORMATION:
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       Davis, Maria
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                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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90071-2066
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       APPLICANT
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                                                     ELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGL---- 454
                                                                                                                                                                      -----QPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHE 498
                                                                                                                                                                                          499 FGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADD 558
                                                                                                                                                                                                                                                                         ------NVHIDKVKLS-----FWDGQDTSKPAENFKDGSLTAAR 258
                                                                                                                                                                                                                                                                                                           559 L------LEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAK----- 602
                                                                                                                                                                                                                                                                                                                                                                                  ------YCSEILGVAATP----GTNMPATFGHLAGGYDGOY-----YGY 636
                                                                                                                                                                                                                                                                                                                                                                                                                 319 KDFRQAIAFGFDRTAYASQINGQTGASKILRNLFVPPTFVQADGKNFGDMVKEKLVTYGD 378
23 YETDPDNLNYLTTAKAATANITSNVVD-----GLLENDRYGNFVPSMAEDWSVSKDG 74
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BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47, Application US/08600993A
Sequence 47, Application US/08600993A
Patent No. 5981299
APPLICANT: Pearce, Barbara J
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: ACELULAR VACCINES BAS
TUNBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-069 US TELECOMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1-MAR-1996
CLASSIRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIRICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY AGENT INFORMATION:
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379 EWKDVNLAD-----SQDGLYNPE 396
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
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TELEX: 133521
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US-08-600-993A-47
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                                                                                                                                                                                                                                                                      296 YSTHADFVLEMNTAK-STSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDG 354
                                                                                                                                                                                                                                                                                           23 YETDPDNLNYLTTAKAATANITSNVVD-----GLLENDRYGNFVPSMAEDWSVSKDG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------YGYDGY----YCSEILGVAATP----GTNMPATFGHLAGGYDGQY-----YGY
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                                                                                                                                                                                                                             Indels 149;
                                                                                                                                                                                    Length 643;
                                                                                                                                                                                  Query Match 3.1%; Score 113.5; DB 2; Best Local Similarity 19.4%; Pred. No. 0.095; Matches 86; Conservative 57; Mismatches 152;
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Job time: 792 sec
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                                        : 643 amino acids
amino acid
INFORMATION FOR SEQ ID NO:
                     SEQUENCE CHARACTERISTICS
                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-600-993A-47
                                          LENGTH:
                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
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